1-1-1978

Estimation of genetic population parameters for a mating appraisal program

John Russell Thompson
Iowa State University

Estimation of genetic population parameters for a mating appraisal program

by

John Russell Thompson

A Thesis Submitted to the
Graduate Faculty in Partial Fulfillment of
The Requirements for the Degree of
MASTER OF SCIENCE

Department: Animal Science
Major: Animal Breeding

Iowa State University
Ames, Iowa

1978

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

INTRODUCTION

The purpose of this study is to estimate genetic parameters for the Mating Appraisal for Profit (MAP) program of Midwest Breeders Cooperative. This program is one of several corrective mating programs presently in use by major artificial insemination organizations. The major purpose of these programs is to produce superior progeny by selective mating procedures. The intent of these programs is to produce progeny which are structurally sound and, thus, will have longer productive lives as opposed to progeny not produced by selective mating.

The question each farmer must answer is, will this program result in sufficient returns from a longer productive life to offset the cost of appraisal? This study will attempt to establish the genetic basis for improvement. Estimation of heritabilities of all traits in the program is the first step in establishing this basis. If the heritability of any or all traits is small, the rate of genetic improvement resulting from selection will be slow. Larger heritabilities indicate that the rate of genetic improvement can be accelerated, however unfavorable genetic correlations can cause problems for overall genetic improvement. This study will also estimate these parameters. If the program is to be of value, genetic correlations must not reflect a loss in one trait coupled with a gain in a second trait.

The MAP program presently in use was based on the results of an earlier study by Aitchison (1971). This study will use an improved model to re-estimate the parameters reported by Aitchison. This study will also

estimate parameters for improvements suggested by Aitchison and attempt to evaluate the usefulness of the improvements.

The work of Aitchison will also provide the major source of review for the present study. Results from the Holstein-Freisian program will also be reviewed. Because different programs do not always evaluate the same traits, although the names are equivalent, the work of Aitchison is the better source.

REVIEW OF LITERATURE

Different type appraisal programs have different goals, thus the criteria used in scoring varies from program to program. Since the purpose of the MAP program is to evaluate cows on functional type while the purpose of the official Holstein-Friesian Association of America (HFAA) program is to evaluate cows with respect to an ideal, the results of the programs may vary. However, as the ideal cow and the functional cow are hopefully the same, results from one program should corroborate results from the other. Most previous work on type has used data from the official HFAA program, thus most results reported will be from this program. A major source of information for the present study is the earlier analysis of the Mating Appraisal for Profit (MAP) program of Midwest Breeders Cooperative.

Prior MAP Analysis

Aitchison (1971) analyzed a set of MAP data collected between October 1, 1969 and June 1, 1970. At the time of data collection cows were scored on thirteen traits, most of which are the same or similar to the twelve traits in the present study (Table 1). A detailed description of the traits in the present study is given in the following section, Description of Data. Examination of the differences shows that the coding of basic form has been rearranged to a linear order and the old single score for feet and legs has been split into separate scores for each trait. One trait, teats, has been added to the program while three traits, size,

Table 1. Comparison of traits in the MAP program evaluated by Aitchison versus the present MAP program

Aitchison (1971)		Present data	
	Basic form		Basic form
scored	1. medium	scored	1. very angular
	2. slightly angular		2. slightly angular
	3. slightly thick		3. medium
	4. very angular		4. thick
	5. very thick		5. very thick
	All other traits scored for both data sets		
1. outstanding; 2. above average; 3. average; 4. below average; 5. undesirable			
	size		-
	scale		scale
	front		front
	body		body
	top		back
	legs and feet		legs
	-		feet
	rump		rump
	rear udder		rear udder
	fore udder		fore udder
	center support		center support
	-		teats
	disposition		-
	milkout		-

disposition, and milkout, have been eliminated. The traits, disposition and milkout, were, for the most part, owner scored.

The old program also contained a production code and a management code for each herd. The area from which the data were collected was divided into thirteen sales districts with each sales district divided into technician areas. Aitchison (1971) found little variation due to sales districts, .48 to 7.21 percent of the total variation, and technicians areas, 2.66 to 9.59 percent of the total variation. These breakdowns have since been dropped from the program. Also subscores now given to some traits were not in use at the time Aitchison's data were collected.

Before analysis basic form was recoded to follow the same linear arrangement used in the present MAP program. The data Aitchison used were then analyzed using Method II of Henderson (1953) for variance component estimation. This method involves first fitting a model containing any fixed effects, adjusting for the fixed effects, then estimating components of variance. In the case of Aitchison, the model was:

$$Y_{ijkl} = u + E_i + C_j + P_k + (EC)_{ij} + (EP)_{ik} + (CP)_{jk} + e_{ijkl}$$

where

Y_{ijkl} = an observation on the lth cow with the kth production code in a herd with the jth condition code and scored by the ith evaluator

E_i = effect of the ith evaluator

C_j = effect of the jth condition code

P_k = effect of the kth production code

$(EC)_{ij}$, $(EP)_{ik}$, and $(CP)_{jk}$ are interaction of the main effects.

The data were then adjusted for evaluator effects by subtraction of the least squares constants obtained above from the original data. A second analysis was then run on the adjusted data, in this case an among and within sire analysis. The mean squares obtained from the second analysis were then equated to their expectations and variance components calculated. After completing the above steps heritabilities were calculated using the formula $\hat{h}^2 = 4\hat{\sigma}_s^2/\hat{\sigma}_p^2$ where $\hat{\sigma}_s^2$ is the estimated sire component and $\hat{\sigma}_p^2$ is the estimated phenotypic variance $(\hat{\sigma}_s^2 + \hat{\sigma}_e^2)$. At the time of analysis, effects of parity (lactation number), and stage of lactation could not be adjusted for as such information was not recorded. These items have since been added to the program.

Variation Due to Herds

Dickinson et al. (1976) suggests that the differential use of high P.D. bulls in different herds causes these herds to experience differential rates of genetic progress. Because of these differential rates of progress dairy cattle can no longer be considered a single population, but rather several subpopulations with different breeding goals. Over time these differential rates of progress will cause larger and larger subpopulation differences, thus these differences should be adjusted for.

Aitchison (1971) did not adjust for herd differences but did adjust for the production and condition codes assigned to each herd. Just how effective these codes are in removing herd differences is hard to evaluate because of their discrete nature and the subjective manner in which they were assigned. Sires were, however, used in many herds so herds and sires were not directly confounded though partial confounding could have existed.

Working with official Holstein-Friesian type data, Vinson et al. (1976a) reported that herd differences accounted for 1.3 to 3.5 percent of the total variation in the twelve descriptive traits. The same study reported that the herd by sire interaction accounted for 1.3 to 6.4 percent of the total variation. These variance components were calculated using Method I of Henderson (1953), in this case the random effects were included in the model and the fixed effects ignored. Estimates were calculated from over 78,000 observations and should be very accurate for the program in question. It should be noted, however, that herds participating in an official program might pay more attention to type while herds participating in an unofficial program may have varying goals and, thus, show more variation.

Rennie et al. (1974) analyzed 51,000 records obtained from Canadian Holsteins and found herd differences accounted for 3.4 to 10.3 percent of the total variation in eleven breakdown scores of type. The herd by sire interaction was very small accounting for -0.8 to 4.1 percent of the variation. As with all interaction estimates obtained from data with only a small proportion of the herd-sire cells filled, the accuracy of the estimates can be questioned.

The studies of Norman and VanVleck (1970), Hansen et al. (1969), Specht et al. (1967), Carter et al. (1965), and VanVleck (1964) have all reported that herd effects account for less than 10 percent of the total variation in type traits (Table 2). In contrast, Legates (1971) analyzed classification data by four different age groups and reported herd effects accounted for 13 to 25 percent of the variation in overall score. The

Table 2. Summary of percent of total variation due to herd effect from the literature

	Percent of total variation due to	
	Herds	Herd x evaluator interaction
Norman and VanVleck (1970)	0.0 to 10.0	
Hansen et al. (1969)	2.1 to 8.3	
Specht et al. (1967)	5.1 to 8.3	4.3 to 7.6
Carter et al. (1965)	8.0	
VanVleck (1964)	10.0	

herd by sire interaction was found to account for 0 to 8 percent of the total variation, which agrees with results of other studies.

Variation Due to Classifiers

Benson et al. (1951) found a correlation of .56 for the same classifier on different dates, .61 to .76 for different classifiers at the same time, and .48 for different classifiers at different times. Touchberry and Tabler (1951) found corresponding correlations of .40, .62, and .37. The higher correlation for different classifiers on the same date versus the same classifier on different dates shows that changes in the cow from one date to the next are more important than differences in the ideals of the classifier. Aitchison (1971) provides a more thorough review of the repeatability of type classification by the same man on different dates, different men on the same date, and different men on different dates.

Analyzing the first set of MAP data, Aitchison (1971) found significant evaluator differences at the .01 level for scale, front, body, feet

and legs, fore udder, rear udder, center support, disposition and milkout. All other traits were found to be nonsignificant at the .05 level. However, one should not assume that nonsignificance implies no evaluator differences.

In practice, the magnitude of differences and not statistical significance or nonsignificance is important. Least squares constants for evaluators ranged from -.32 to .34 with most having an absolute magnitude of less than .20. In general, these constants are small, the largest being .4 standard deviations for fore udder.

Wilcox et al. (1959) analyzed descriptive type data obtained from New Jersey Agricultural Experimental Station cattle coded one to six. Least square constants for evaluators ranged from -1.31 to 1.46. These constants are much larger than those reported by Aitchison (1971) and suggest evaluator differences are large.

Working with official HFAA classification data Vinson et al. (1976a) found that evaluators account for between 1.4 to 5.0 percent of the total variation in descriptive traits. Using first classification scores Specht et al. (1967) found that evaluators account for 2.8 to 6.0 percent of the total variation in descriptive traits. Both these studies indicate evaluator differences are small, in both cases being about half the magnitude of herd differences. Specht et al. (1967) found the variation due to herd by classifier interaction, 4.3 to 7.6 of the total variation, to be greater than the variation due to classifiers.

Variation Due to Age and Stage of Lactation

Rennie et al. (1974) analyzed official HFAA classification data to determine the effect of age at first classification, stage of lactation, and season of calving. Stage of lactation was fit as the number of months the cow was in milk at the time of classification. Age effects were found to be significant at the .01 level for all descriptive traits except feet and legs, feet and legs being nonsignificant at the .05 level. Stage effects for all descriptive traits were significant at the .01 and all season effects were significant at the .01 level except rump which was significant at the .05 level. The study did not report any trend in scores as a cow proceeded through her lactation (stage effects), in other words, in what periods she scored high and in what periods she scored low.

An analysis of final score and the four breakdown traits, general appearance, dairy character, body capacity and mammary system, of the official HFAA classification program by Hansen et al. (1969), showed highly significant (.01 level) effects of age at classification and stage of lactation scored as months in milk. The interaction of age and stage was nonsignificant at the .05 level. Norman and VanVleck (1970) also found apparent age and stage effects with a small interaction.

Hansen et al. (1969) reported that for all traits except dairy character cows were scored higher at the beginning and the end of their lactation while the seventh month produced the lowest scores. This type of result suggests a quadratic effect of days in milk if fit as a regression instead of a constant. Cows were scored higher on dairy character at the

beginning of their lactation and lower at the end of lactation. This result suggests a linear effect of days in milk if fit as a continuous variable.

Wilcox et al. (1959) analyzed official HFAA type data using six age groups; 1, 2, 3, 4, 5 and 6+ years; and three stage groups; 0 to 60 days in milk, 61 to 240 days in milk and 241 days in milk to the subsequent parturition. Final score and the four breakdowns were found to improve as a cow matured. Wilcox et al. (1959) asks, "Do cows actually improve in rating or is the increase only in the eyes of the classifier?" Ratings might also increase with age because of culling cows on type. Cows were found to score higher in the early and late periods and lower in the middle period. Again, these results suggest a quadratic effect of days in milk when fit as a continuous variable.

All previous work reviewed has analyzed stage of lactation by defining periods and fitting these periods as fixed effects. This method loses information supplied by the variable days in milk by breaking the information into discrete classes. The work of Hansen et al. (1969) and Wilcox et al. (1959) suggests that both linear and quadratic effects of days in milk should be fit in any future work.

Heritabilities of Type Components

Heritability is defined by Falconer (1960) as the ratio of the additive genetic variance to the phenotypic variance or the regression of breeding value on phenotypic value. Falconer (1960) lists four methods for estimating this ratio: 1) offspring and one parent, 2) offspring and

mid-parent, 3) half-sibs, and 4) full-sibs. The best method depends on the nature of data available with half-sib correlation and the regression of offspring on father usually being the most reliable. This ratio will vary from trait to trait within a population and from population to population for any one trait. The criteria used to evaluate any trait can also effect the estimate of heritability.

Most estimates of heritability have been estimated from official HFAA classification data. These estimates are specific to the population of cows used in the study, but can be used as an indicator of estimates to be obtained from other populations. Estimates from official classification programs may also be biased by selective culling of cows for poor type.

In the earlier MAP analysis, Aitchison et al. (1972) estimated heritabilities as in Table 3 using the half-sib correlation method of Falconer (1960). Basic form (.50) was found to be highly heritable in this study. As basic form is a trait unique to the Midwest program other studies provide no estimates for comparison.

Aitchison et al. (1972) found the mammary traits fore udder (.26), rear udder (.26) and center support (.19) to be moderately heritable. Cassell et al. (1973) and White and Vinson (1976) used the regression of offspring on one parent method to estimate heritabilities for the components of the official HFAA classification program. In both studies, all mammary traits were found to be moderately heritable (Table 3) ranging from .20 to .24. Estimates of both studies were extremely accurate having standard errors of .01 or smaller. Johnson and Fourt (1960) using a much smaller and therefore less accurate sample reported slightly higher

Table 3. Summary of heritability estimates from the literature

	Aitchison (1971)	Cassell et al. (1973)	O'Bleness et al. (1960)	Norman and VanVleck (1970)	Johnson and Fourt (1960)	Rennie et al. (1974)	White and Vinson (1976)
Basic form	.50	-	-	-	-	-	-
Scale	.39	.48	-	.39	-	-	.51
Front	.25	.15	-	-	-	-	.12
Body	.36	.27	-	.17	.24	.31	.27
Back	.22	.17	-		-	-	.23
Legs	-	.08	.08		-	-	.15
Feet	-	.11	-		-	-	.11
Rump	.23	.24	-		.39	.33	.25
Rear udder	.23	.20	.30		.35	-	.21
Fore udder	.26	.20	.16		.29	.15	.21
Center	.26	.23	-		-	.14	.21
Teats	-	.24	.09 to .05		-	-	.31
Feet & legs	.33	-	-		.20	.07	-
Udder traits				-.02 to .16			

heritabilities of .23 and .35 for fore and rear udder, respectively. In contrast, Norman and VanVleck (1972) analyzed 21 mammary traits of which only nine had heritabilities greater than .10 with none grater than .16. O'Bleness et al. (1960) and Rennie et al. (1974) reported similar findings (Table 3).

All studies reviewed reported heritabilities of feet and legs much smaller than those of Aitchison (1971). The findings of Cassell et al. (1973), White and Vinson (1976), Norman and VanVleck (1972), Rennie et al. (1974) and O'Bleness et al. (1960) ranged from .07 to .15 and are listed in Table 3.

The estimates of the heritability of front end reported by White and Vinson (1976) (.12) and Cassell et al. (1973) (.15) are both considerably lower than Aitchison et al. (1972) (.25). Heritability estimates for scale, body, back and rump obtained by Aitchison (1971) tend to agree with the estimated obtained by other studies (Table 3); the only exception being Norman and VanVleck (1972) .09 for back is some what lower than all other studies.

In general, most previous work has shown feet and legs to be lowly heritable; the udder traits plus front, top and rump to be low to moderately heritable; the structural traits scale, body and size to be moderately to highly heritable; and basic form to be highly heritable.

Genetic and Phenotypic Correlations

Genetic correlation can be looked at as an indicator of how one trait will change with selection on a second trait. A highly positive correla-

tion suggests that selection on one trait will produce improvement in the correlated trait. Falconer (1960) gives the formula for expected correlated response as:

$$CR_y = ih_x h_y r_A \sigma_{p_y}$$

where

CR_y = the correlated response of trait Y when selecting for trait x

i = the intensity of selection for x

h = square root of the heritability of the subscripted trait

r_A = the genetic correlation between x and y

σ_{p_y} = phenotypic standard deviation of trait y

Phenotypic correlation is the observable relationship between two trait which may or may not be adjusted for environmental effects. A summary of some of the phenotypic correlations from the literature as in Table 4.

Aitchison et al. (1972) reported phenotypic but not genetic correlations. All traits were negatively correlated with basic form. Keeping in mind the scoring system these correlations imply that a very angular cow would tend to score poor in the correlated trait while a thick cow would tend to score desirable in the correlated trait. Other correlations were positive but small usually less than .20 and often less than .10 (Table 4). Inspection of the results shows that two groups of traits tend to be highly correlated: 1) the three udder traits showed larger correlations with each other and 2) scale (.58), front (.35) and body (.39) were all highly correlated with size.

Table 4. Estimates of phenotypic and genetic correlations from the literature[a]

	Body	Stature	Front	Back	Rump	Legs	Feet	Fore udder	Rear udder	Center support
Body		.77[b]	.95	.44	.42	.46	.44	.26	.20	.16
		-[c]	-	-	.47	.35	.35	.41	.44	-
		-[d]	-	-	.80	.86	.86	.76	.86	-
		-[e]	-	-	-	-	-	-	-	-
Stature	.51		.62	.29	.25	.24	.31	.13	.13	.06
	-		-	-	-	-	-	-	-	-
	-		-	-	-	-	-	-	-	-
	.04		-	-	-	-	-	-	-	-
Front	.54	.34		.47	.51	.39	.32	.20	.32	.11
	-	-		-	-	-	-	-	-	-
	-	-		-	-	-	-	-	-	-
	.26	.17		-	-	-	-	-	-	-
Back	.20	.20	.25		.34	.16	.11	.10	.10	.09
	-	-	-		-	-	-	-	-	-
	-	-	-		-	-	-	-	-	-
	.13	.08	.10		-	-	-	-	-	-

[a]Genetic correlations above diagonal and phenotypic correlations below diagonal.

[b]Estimate of Cassell et al. (1973).

[c]Estimate of Rennie et al. (1974).

[d]Estimate of Johnson and Fourt (1960).

[e]Estimate of Aitchison (1971).

Table 4. (Continued)

	Body	Stature	Front	Back	Rump	Legs	Feet	Fore udder	Rear udder	Center support
Rump	.26	.19	.25	.26		.48	.19	.16	.31	.13
	.19	-	-	-		.30	.30	.38	.53	-
	.34	-	-	-		.54	.54	.67	.54	-
	.14	.07	.14	.19		-	-	-	-	-
Legs	.20	.12	.19	.10	.20		.11	.22	.07	.13
	.12	-	-	-	.13		-	.46	.52	-
	.25	-	-	-	.24		-	.57	.58	-
	.03	.11	.12	.10	.07		-	-	-	-
Feet	.18	.13	.16	.08	.13	.24		.30	.18	.18
	.12	-	-	-	.13	-		.46	.52	-
	.25	-	-	-	.24	-		.57	.58	-
	.03	.11	.12	.10	.07	-		-	-	-
Fore udder	.14	.11	.14	.11	.18	.09	.10		.50	.42
	.14	-	-	-	.15	.10	.10		.55	-
	.36	-	-	-	.32	.20	.20		.74	-
	.03	.05	.08	.00	.08	.09	.09		-	-
Rear udder	.18	.14	.18	.11	.22	.15	.12	.25		.38
	.13	-	-	-	.20	.14	.14	.36		-
	.32	-	-	-	.53	.24	.24	.44		-
	.03	.05	.10	.00	.13	.15	.15	.47		-
Center support	.08	.04	.06	.04	.09	.05	.05	.25	.25	
	-	-	-	-	-	-	-	-	-	
	-	-	-	-	-	-	-	-	-	
	.02	.01	.03	.03	.05	.06	.06	.39	.28	

In general, these results agree with the work of Rennie et al. (1974), but are smaller than those reported by Atkeson et al. (1969), Cassell et al. (1973) and Johnson and Fourt (1960). Results reported by Atkeson et al. (1969) ranged from .21 to .56, those of Cassell et al. (1973) ranged from .05 to .54 with most between .10 to .30 and those of Johnson and Fourt (1960) ranged from .17 to .80 (see Table 4 for complete results). All above studies showed large correlations for characters in close physical proximity (i.e., teats with center support) and smaller correlations for traits not in close proximity (i.e., teats with front).

Johnson and Fourt (1960), Cassell et al. (1973) and Rennie et al. (1974) all reported genetic correlations to be larger than phenotypic correlations. Cassell et al. (1973) found all genetic correlations to be positive ranging between .06 (body-support) to .95 (front-body). Johnson and Fourt (1960) and Rennie et al. (1974) also found all genetic correlations to be positive some of which were also extremely large (.80 and above). Again all traits in close proximity showed large correlations while traits not in close proximity showed small correlations. The results obtained by Johnson and Fourt (1960) using a small data set were in general larger than results of the other studies. White (1974) also provides a review of heritabilities of type components.

Subscores and their Heritabilities

Because of their descriptive nature, subscores require special attention in any analysis. One of several possible subscores can usually be assigned to each trait. Each of these categories attempts to describe the

exact nature of the fault for the trait in question. As an example, for legs a cow might be assigned subscore one if her legs are too straight, subscore two if her legs are too sickled, or subscore three if her hocks turn in. These scores do not run in any linear fashion as it cannot be said a subscore of two is worse than a one, but better than a three.

With these problems in mind VanVleck (1964) analyzed data collected by extension personnel in New York. Each of several traits was assigned a subscore describing the nature of the fault for the trait in question, if any. Each separate subscore category within a trait was then coded as a binomial; 0 = not present, 1 = present. If a cow was assigned subscore 3 of three possible categories for trait legs three new variables would be created coded 0, 0, and 1. The recoded data were then analyzed. The subscores for most body traits were found to be low to moderately heritable ranging from 10 to 20 percent. Heritabilities of the subscores for udder traits were slightly higher ranging from 10 to 30 percent heritable. The work of Hillers and Everson (1972) has shown that breaking a normal distribution into discrete subclasses can greatly affect the magnitude of heritability depending on the amount of skewedness the discrete subclasses introduce. These results should be kept in mind when interpreting the heritabilities of subscores estimated by VanVleck (1964) as the coding method causes a large amount of skewing toward zero.

LaSalle et al. (1973) coded the subscores used in the official HFAA classification program in the same manner as VanVleck (1964). Heritabilities were then calculated and the results corrected for the effect of discontinuity using the methods of VanVleck (1972). High heritabilities

(.36 to .83) were found for "low set in stature," "sloping rump," "too straight hind legs," "broken rear udder," "rear teats too far back" and several others. Progress can be expected in trying to correct these specific faults because of their high heritability. In contrast, most udder quality subscores had low heritabilities ranging from .00 to .10.

Usefulness of Mating Appraisal

The ultimate purpose of most dairy operations is to make money. Thus, for a mating appraisal program to be useful to the average dairyman it must either increase his production, cut down on his replacement costs by allowing cows to stay in the herd longer or increase the value of his animals sold as replacements.

A symposium on type conformation can be found in the Journal of Dairy Science, volume 57, pages 1267-1284. The symposium describes the industry and the producers' views on type confirmation. In the same symposium, White (1974) lists eight research needs in type conformation, one of which is to evaluate the value of mating appraisal programs such as the MAP program. The symposium again stresses that for appraisal programs to be useful they must increase returns in some manner.

Aitchison et al. (1972) found that most phenotypic correlations between type components and production were small, most being negative. Because of the scoring system used, negative correlations imply that more desirable cows produce more milk. However, only scale (-.08) and body (-.09) showed significant correlations at the .05 level.

Johnson and Fourt (1960) found genetic correlations between type components (body, fore udder, rear udder, feet and legs, and rump) with fat production were all positive ranging from .21 to .48. Harvey and Lush (1952) estimated the genetic correlation between overall type and milk fat production to be .18. Wilcox et al. (1971) found the genetic correlation between milk production and fat production to be .70, thus, without calculating partial correlations these results seem to indicate a positive correlation between type and production.

White and Vinson (1976) found all traits in the official HFAA classification program were negatively correlated with PD milk except dairy character, which was highly positive (.41). Under the official scoring system, a negative correlation would imply better type yields less milk. Comparing this with the better score more milk relationship of Aitchison et al. (1972), different goals may indeed exist between the two programs. Also most older data indicated a positive relationship between type and production while more recent studies using larger volumes of data have found a negative relationship.

Granthom et al. (1974) reported small negative genetic correlations between type and production. Phenotypic correlations reported by the same study ranged from -.14 to -.16 for the scoreboard traits except dairy character (0.38) and -.02 to +.22 for the descriptive traits. Other studies, Freeman and Dunbar (1955) and Butcher et al. (1963), reported similar results. From these results, genetic correlations between milk or milk fat and type seem to be small or negative for most type components, thus little improvement in production can be expected from selection on type.

However, if cows do stay in herds longer because of better type, replacement costs would be reduced and more voluntary culling on production would be possible. Specht et al. (1967) found the correlation between first type score and herd life to be .20. In the same study, number of times classified used as a measure of herd life was found to have a small regression coefficient (.10). These studies seem to indicate that better type allows cows to stay in herds longer. However, in a personal communication, Everett reported a negative correlation between final score and length of herd life.

Allaire et al. (1977) analyzed reasons given for culling by age group. Type was found to be the most frequent reason for removal of six to fifteen month old animals (49%). Prior to first calving type was found to account for 24.4 percent of the primary and 55.1 percent of the secondary reasons for culling. After calving, type was found to account for only 3.4 percent of the primary and 17.2 percent of the secondary reasons for culling. These results suggest that most animals culled for type are removed before calving, thus, the animals are never given a chance to show their producing ability. VanVleck and Norman (1972) analyzed the reasons for disposal of 3,475 New York Holsteins reporting 3.1 percent were disposed of for type and 23.4 percent for udder problems of which 5.1 percent could be attributed to udder type. Their results suggest that selection to improve type might cut down on replacements, but to a fairly small extent.

There is little doubt that high classifying cows bring more money than low classifying cows. An analysis of 1958 sales of Holstein cattle

by Prescott et al. (1960) showed the average prices of classified females as follows: excellent - $1,139, very good - $706, good plus - $542, good - $461, and fair - $369. The study also reports the average price for classified cows was $521.21 versus $381.29 for unclassified cows.

The true test of any mating appraisal program is does it increase net income? Although no studies have looked at this question the growth of the MAP program, dollar volume was 46.3 percent higher in 1976 compared to 1975, would seem to indicate the dairyman believes the program works.

DESCRIPTION OF DATA

A data set containing 15,594 observations collected between July 1, 1975 and March 31, 1976 was supplied by Midwest Breeders Cooperative. The data were collected by Midwest Mating Appraisal for Profit (MAP) specialists from herds in Iowa, Minnesota, Missouri, Nebraska, and Wisconsin. The purpose of the program is twofold: 1) to help the dairyman in choosing bulls for matings and 2) to provide type information on Midwest bulls.

The MAP program is provided as a service to both the dairyman and the cooperative. Because of this only a small fee is charged to cover the expenses of the specialist. For all herds not previously scored, a minimum of twenty-five cows must be evaluated. Repeat herds are required to have a minimum of fifteen cows. Previously scored cows can be re-evaluated at subsequent herd evaluations, however, a fee is only charged if the evaluator makes a change in the previous scoring.

The evaluator first records the identity of the sire and dam of the cow evaluated along with her parity (lactation number) and current days in milk. The practice of identifying the sire prior to scoring might induce bias into the evaluation. Sire identification after scoring would be a preferable technique. Heifers and dry cows are scored if the dairyman so requests. The specialist may also inquire about the cow 's present milk and fat production. Fat percentage is considered in choosing the sire recommended for mating.

After recording the above information each cow is scored on twelve components of type defined as:

Basic form: refers to the relative differences between cows for angularity or thickness.

Angular characteristics--long, narrow head; long, lean neck; extreme sharpness of shoulder; narrow chest; tendency to weakness behind shoulder and shallowness of heart and body; prominence of hooks and pins; flat, light bone; flat, clean thighs; general lack of excess tissue; good udder quality.

Thick characteristics--short, wide head; short, thick neck; heavy at top of shoulders; good width of chest and excess brisket; tend toward round, shallow rib; round, heavy bone; thick thighs; tendency to excess tissue throughout; general lack of quality, including udder.

Scoring for basic form: 1. very angular, 2. slightly angular, 3. medium, 4. slightly thick, 5. very thick.

All other traits scored: 1. outstanding, 2. above average, 3. average, 4. below average, 5. undesirable.

Scale: pertains to the overall height or upstandingness of the animal.

Front: includes the head and neck, the shoulders and how they blend to the rest of the body. The height of the shoulders in relation to the rest of the animal. The heart, which includes the width and depth of the chest cavity from the tip of the shoulder to the floor of the chest.

Body: primarily, body includes depth or length of rib in relation to the rest of the animal. Also, spring of rib and length of body which contribute to total capacity is considered.

Back: refers to strength of loin, straightness and strength of back from the hips forward.

Legs: bone flat and strong, hocks cleanly moulded; fore legs medium in length, straight, wide apart, and squarely placed; hind legs nearly perpendicular hock to pastern from the side view, straight from the rear view.

Feet: short, compact and well-rounded with deep heel and level sole. Pasterns short and strong.

Rump: includes hip and pin width. Straightness and flatness of rump. Also, considers height or ridginess, smoothness and degree of coarseness.

Rear udder: width and height of rear udder attachment, general symmetry and rear teat placement. Also, rear udder depth and levelness in relation to the fore udder.

Fore udder: length and attachments to the body wall. Width in relation to the rear udder. Placement of teats and levelness in relation to the rear udder.

Center support: prominence and apparent strength of the center suspensory ligament and halving of the udder. Plumbness of the teats. Includes the overall quality and texture of the udder.

Teats: uniform size, of medium length and diameter, cylindrical, squarely placed under each quarter, plumb, and well-spaced from side and rear views.

Any time front, legs, feet, rump, rear udder, fore udder or teats are scored four or five (the two undesirable classifications) a subscore is used to describe the exact nature of the fault. Each trait has its own specific set of subscores, the subscores used in the MAP program are listed below.

Front end: 1. low front, 2. wing shoulders, 3. narrow front, 4. weak crops, 5. coarse.

Legs: 1. too straight, 2. too much set, 3. hocks in, 4. stance, 5. toes out in front.

Feet: 1. shallow heel, 2. spread toes, 3. faulty pasterns, 4. toes curl.

Rump: 1. high tail head, 2. sloping, 3. ridgy, 4. narrow.

Rear udder: 1. low attachment, 2. narrow attachment, 3. uneven curvature, 4. too deep-tilted, 5. too shallow-tilted.

Fore udder: 1. weak attachment, 2. bulgy and loose, 3. too deep-tilted, 4. too shallow-tilted, 5. too short.

Teats: 1. wide front teats, 2. too large or long, 3. poorly shaped, 4. back too far, 5. too close on side, 6. teats strut.

No final score is assigned to an animal in the MAP program in contrast to the official HFAA type classification program. Instead the evaluator uses the scores on the twelve type components along with subscores to correct as many faults as possible by selective mating. Basic form is the first consideration in all recommended matings, angular cows being mated to thick bulls and thick cows to angular bulls (negative assortative mating). Within the basic form limitation the specialist recommends three bulls within the stud known to sire progeny strong in the traits where the dam is weak. The herd owner may or may not impose certain restrictions on the production level or the fat test of bulls recommended if he feels conditions warrant. The herd owner is also free to use other bulls if he disagrees with the specialist.

The data were collected from 422 different herds, each herd scored by one of six specialists. Herd size ranged from five to one hundred and three, most herds having between twenty-six and fifty cows scored (Table 5).

Table 5. Herd distribution of MAP data

Number of observations per herd	Number of herds
0-25	97
26-50	256
51-75	55
76-100	12
100+	2

Over 92 percent of the data were scored by three of the six specialists; numbers 1, 2, and 3; while one specialist, number 6, scored only one herd representing eighty-two observations (Table 6). The initial data were also found to contain 210 different sire identities on 8,581 observations. However, 39 of these codes did not conform to the standard format or were eliminated for reasons to be explained later, thus reducing the number of sires to 171 representing 7,859 individuals, or 50.4 percent of the original data.

Table 6. Number of herds and number of cows scored by each specialist

Specialist	Observations	Number of herds scored
1	3,369	91
2	4,677	115
3	5,992	168
4	957	32
6	82	1
7	517	15

METHODS AND PROCEDURES

Model

To describe the factors affecting evaluation of any type component, a model was chosen which included the effects: herd, evaluator, parity, stage of lactation, sire and error. The number of days in milk, as a continuous variable, was used to describe stage of lactation in the model. As the data included cows in milk, dry cows and heifers the problem of how to code dry cows and heifers for stage of lactation arose. A cow that has just finished her lactation should be coded the same as a cow that is about to finish her lactation while a cow that is ready to calve has an appearance closer to a cow that has just calved. Stage of lactation does not apply to heifers. To alleviate this problem the data were analyzed separately by milk cows, dry cows and heifers. The models used were:

Heifers

$$u + E_i + H_{ij} + S_l + e_{ijl}$$

Dry cows

$$u + E_i + H_{ij} + P_k + S_l + (EP)_{ik} + S_l + e_{ijkl}$$

Milk cows

$$u + E_i + H_{ij} + P_k + (EP)_{ik} + S_l + b_1\ (DIM) + b_2(DIM)^2 + e_{ijkl}$$

where

u = the underlying population mean

E_i = the effect of the ith evaluator

H_{ij} = the effect of the jth herd scored by the ith evaluator

P_k = the effect of the kth parity

$(EP)_{ik}$ = the interaction of the ith evaluator with the kth parity

S_l = the effect of the lth sire

e_{iykl} = an error term which is normal independently distributed with mean zero, variance σ^2

DIM = the number of days in milk for the record being analyzed

These models were applied to both the type components and the subscores.

Data Preparation

Each data subset was edited to eliminate any problems which might arise in statistical analysis. Because evaluator number six scored only one herd his effect was confounded with the effect of the herd which he scored, thus, all data scored by evaluator six were eliminated from the data subsets. For the milk cow and dry cow data subsets parity was recoded one through four, and five and greater. This recoding allowed all cells in the evaluator by parity interaction to be filled yielding a more precise estimate of the interaction along with a smaller X'X matrix. The recoding was done under the assumption that once a cow has matured her score will remain constant. This assumption probably would be false for older cows because of excessive wear and tear, however, very little information was available on older cows (only seven cows were parity ten or greater).

Last, to avoid confounding of a sire's effect with a herd's effect all single herd sires were eliminated from the data. All data with a non-Holstein sire were also edited as breeds tend to be confounded with herds. Non-Holstein sires represented a small proportion of the total data. The

above edits left 533 observations and 31 sires in the heifer subset, 1000 observations and 48 sires in the dry cow subset, and 6372 observations and 102 sires in the milk cow subset.

Because of the nonlinear nature of subscores it was necessary to recode each separate subscore code as present or not present. After consulting with Midwest MAP specialists a trinomial coding system was chosen over the binomial system used in the HFAA classifications analysis. This was done to indicate the degree of severity of the fault or subcode. This process required the editing of the data into seven single trait subsets, one for each trait for which subscores were employed. Each subscore subset consisted of all obervations scored four or five on the type component used for building the subset. All other observations were edited out of the data because a certain fault might be present but not severe enough for the type component to be scored undesirable. All data, however, were used in the main analysis, which ignored subscores. The seven subsets were not mutually exclusive because any one cow might have more than one undesirable type component.

Each separate subscore subset was then coded so that each record had as many trinomial scores as the number of possible subcodes used for the type component. Thus, for feet with four subcodes four trinomial scores would be employed, one for each subcode. These four codes represent the phenotype of the cow and were used for analysis. The trinomial score for the subcode used was coded two if the component score was four and three if the component score was five. All other subcodes would be unused for the record and the trinomial score was coded one, not present. Thus, if

the component score for feet was four with subcode three the trinomial scores were coded one, one, two, and one. A sample data set with one type component and three possible subcodes is coded in Table 7.

Table 7. An example of the trinomial coding of subscore data

Animal No.	Component score	Subcode	Trinomial scores for subcode[a]		
			1	2	3
1	4	2	1	2	1
2	5	1	3	1	1
3	3	-	-	-	-
4	2	-	-	-	-
5	4	3	1	1	2

[a]Each record analyzed would have three scores.

The subscore data were edited in the same manner as the type component data.

Analysis Procedure

After editing the data were analyzed using a complete least squares analysis. Because of the large number of herds in the data, herd effects could not be solved for directly as inverting the resulting X'X matrix would be computationally infeasible. An algebraic process known as absorption was used to remove herd effects. The data structure required both herd and evaluator effects to be absorbed in this analysis because only one evaluator scored each herd.

The absorption procedure consists of solving the least squares equations for herds in terms of the other effects in the model. The result is then substitued into the remaining least squares equations. Lentz et al. (1969) showed by example how absorption could be accomplished as herds were read into the computer sequentially.

For the heifer model the coefficients after absorbing herds would be:

$$C = \begin{bmatrix} \sum_i (n_{i1.} - \frac{n_{i1.}^2}{n_{i..}}) & -\sum_i \frac{n_{i1.} n_{i2.}}{n_{i..}} & \cdots & -\sum_i \frac{n_{i1.} n_{ip.}}{n_{i..}} \\ -\sum_i \frac{n_{i2.} n_{i1.}}{n_{i..}} & \sum_i (n_{i2.} - \frac{n_{i2.}^2}{n_{i..}}) & & \vdots \\ \vdots & & \ddots & \\ -\sum_i \frac{n_{ip.} n_{i1.}}{n_{i..}} & \cdots & & \sum_i (n_{ip.} - \frac{n_{ip.}^2}{n_{i..}}) \end{bmatrix}$$

where

$n_{i1.}$ = the number of records of the k sire in the ith evaluator-herd subclass

$n_{i..}$ = the total number of records in the ith herd

p = the number of sire

C = X'X matrix after absorption

The absorption procedure must also be performed on the right hand sides. The absorbed right hand side matrix would be:

$$RHS = \begin{bmatrix} \sum_i (Y_{i1.} - n_{i1.} \bar{Y}_{i..}) \\ \sum_i (Y_{i2.} - n_{i2.} \bar{Y}_{i..}) \\ \vdots \\ \sum_i (Y_{ip.} - n_{ip.} \bar{Y}_{i..}) \end{bmatrix}$$

where

$Y_{il.}$ = the sum of observations for the daughters of the kth sire

$Y_{i..}$ = the mean of all observations in the ith herd

In the case of the MAP program, scores are available on twelve type components, thus, this study made use of multiple right hand sides. The right hand side matrix for the MAP analysis was p x 12 rather than p x 1 as in the above example. The use of multiple right hand sides allows for the calculation of not only the sum of squares for each trait, but also all possible cross products between traits. To minimize the accumulation of rounding errors all calculations were done in double-precision FORTRAN (14 significant digits in most cases).

The present study accomplished the absorption process by reading in the data sorted in evaluator-herd sequence one record at a time. The least squares equation was then built for each record and accumulated in a half-stored matrix. At the same time the right hand side matrix was accumulated along with all herd-effect ($n_{il.}$) frequencies and the overall herd frequency. A within herd sum of squares was also accumulated as the data were read in. This was accomplished by accumulating a total sum of squares for the herd and then subtracting the correction factor for the herd from the total. The corrected total, herewith called the within herd sum of squares, was then accumulated over all herds. When the end of an evaluator-herd subclass was sensed the algebra of the absorption was carried out as shown by Rindsig (1976). The process was then repeated for each subsequent evaluator-herd subclass until all data had been passed. At this point, the X'X matrix would be of order q, the total number of levels summed over all nonabsorbed effects in the model. Such a matrix

would be singular, thus, some type of restriction was required which would yield a nonsingular matrix. For this analysis, the sum of the estimates for all levels of each effect was forced to sum to zero. That is: $\Sigma_k P_k = 0$ and $\Sigma_l s_l = 0$ for the main effects of parity and sire and $\Sigma_i (E * P)_{ik} = 0$ and $\Sigma_k (E * P)_{ik} = 0$ for the interaction of evaluator by parity. After restriction, the X'X matrix should be nonsingular and ready for direct inversion; that is, the matrix should be of full rank r.

After inversion the least squares constant estimates ($\hat{\beta}$'s) were calculated using the standard formula:

$$\underset{rx12}{\hat{\beta}} = \underset{rxr}{(X'X)^{-1}} \underset{rx12}{X'Y}$$

The program then calculates the error sum of squares by subtracting the reduction due to all effects in the model from the within herd sum of squares and cross products:

$$\underset{12x12}{ESS} = \underset{12x12}{WHSS} - \underset{12x12}{R(all)}$$

and

$$\underset{12x12}{R(all)} = \underset{12xr}{\hat{\beta}'} \; \underset{rx12}{X'Y}$$

where

ESS = error sum of squares and cross products

WHSS = with herd sum of squares and cross products

R(all) = reduction due to all nonabsorbed effects in the model

To calculate the sum of squares and cross products due to the other effects in the model and the variance components the $(X'X)^{-1}$ matrix, herewith called Z, was block diagonalized by zeroing out all off-diagonal blocks so that each block consisted of the rows and columns equivalent to each effect:

$$Z = \begin{bmatrix} Z_1 & & & & \\ & Z_2 & & \phi & \\ & & Z_3 & & \\ & \phi & & Z_4 & \\ & & & & Z_5 \end{bmatrix}$$

where

Z_1 = rows and columns for parity (k - 1 x k - 1)

Z_2 = rows and columns for the interaction (i - 1)(k - 1) x (i - 1) (k - 1)

Z_3 = rows and columns for sires (ℓ - 1 x ℓ - 1)

Z_4 = row and column for linear days in milk (1 x 1)

Z_5 = row and column for quadratic days in milk (1 x 1)

Inversion of each block (Z_i) of Z yields the inverse of Z, (Z^{-1})

$$Z^{-1} \begin{bmatrix} Z_1^{-1} & & & & \\ & Z_2^{-1} & & \phi & \\ & & Z_3^{-1} & & \\ & \phi & & Z_4^{-1} & \\ & & & & Z_5^{-1} \end{bmatrix}$$

The inversion of the Z matrix will also yield Z_i^{-1} matrices which are not the equivalent of the subsection in the original X'X matrix in contrast to the usual $(A^{-1})^{-1} = A$, where A is any square matrix.

Harvey (1975) lists the formula to obtain a partial sum of squares and cross products for each effect as:

$$\underset{12x12}{SS_i} = \underset{12xm_i}{\hat{\beta}_i'} \quad \underset{m_ixm_i}{Z_i^{-1}} \quad \underset{m_ix12}{\hat{\beta}_i}$$

where

SS_i = sum of squares and cross products matrix for the ith effect

$\hat{\beta}_i$ = the constant estimates for the ith effect

m_i = number of rows and columns in the Z matrix for the ith effect

Z_i = rows of columns of the $(X'X)^{-1}$ matrix relating to the ith effect

The resulting 12 x 12 SS matrix contains the sum of squares for each trait corresponding to the ith effect on the diagonal and the cross products on the off-diagonal. As with all variance-covariance matrices the SS matrix is symmetric and can thus be half-stored to conserve core.

The Z_i^{-1} matrices are also used in the estimation of variance and covariance components. Parity and evaluator by parity effects were considered fixed while sires were handled as a random effect. The expected mean square then has the form:

Sire $\quad \sigma_e^2 + K_1\sigma_s^2$

Error $\quad \sigma_e^2$

Again, using the methdology of Harvey (1975) the k_1 value was calculated using the formula:

$$k_1 = 1/S_3\left(\sum_j (Z_3^{-1})_{jj} - 1/(S_3 - 1)\sum_{\substack{j \\ j\neq 1}} \sum_1 (Z_3^{-1})_{j1}\right)$$

where

S_i = the degrees of freedom for the ith effect in the model

Note: $\sum_j (Z_i^{-1})_{jj}$ is the sum of the diagonal elements and $\sum_{\substack{j \\ j\neq 1}} \sum_1 (Z_i^{-1})$ is the sum of the off-diagonal elements.

The mean squares obtained from the previous section were then equated to their expectation obtained above and the variance and covariance components

solved for:

$$A_i = (MS_i - E)/k_i$$

where

A_i = variance-covariance components for the ith effect

MS_i = mean square matrix for the ith effect

E = error mean square matrix

Heritability Corrections to the Normal Scale

Vinson et al. (1976b) develops the methodology necessary for adjusting heritabilities obtained from discrete data to their expectation on the normal scale. The methodology assumes the data has an underlying normal or approximately normal distribution with the discrete subclasses being linearly adjacent on the normal scale.

For a multinomial trait with t possible classes the assumed distribution is as in Figure 1.

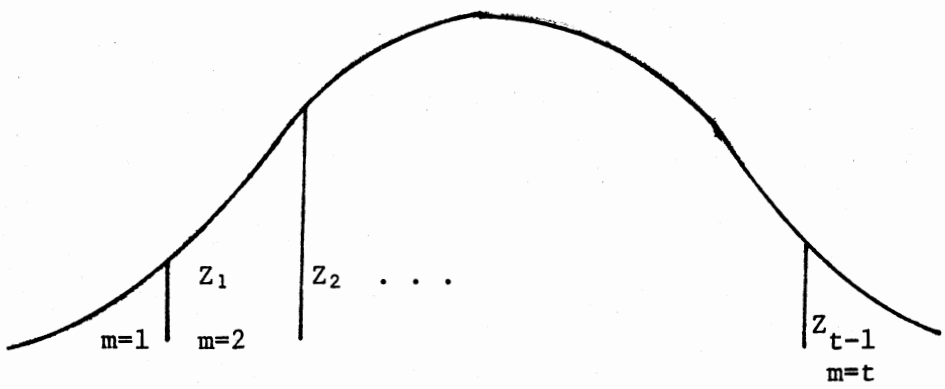

Figure 1. Assumed distribution in correction of heritabilities to the normal scale.

where

m = the class code

Z_i = the height of the curve at the break point for the ith score obtained from a normal ordinate table

Heritabilities obtained from discrete data are then corrected using the formula:

$$\hat{h}_u^2 = \hat{h}_m^2 \hat{\sigma}_m^2 / \left(\sum_i^{t-1} Z_i \right)^2$$

where

$\hat{h}_m^2$ = the heritability estimate on the discrete scale

$\hat{h}_u^2$ = the heritability estimate on the normal scale

$\hat{\sigma}_m^2$ = a variance type estimate calculated as:

$$\hat{\sigma}_m^2 = 1/r \sum_{i=1}^{r} (M_i - \overline{M})^2$$

where

r = number of individuals

M_i = the discrete phenotype for the ith individuals

$\overline{M}$ = the mean for ith trait

Vinson et al. (1976b) also shows the genetic correlation obtained from discrete data and the expectation on the normal scale are equivalent. The relationship between a phenotypic correlation estimated from discrete data and the expectation on the normal scale is:

$$\hat{p}_{uv} = \hat{p}_{mn} \hat{\sigma}_n \hat{\sigma}_m / \left(\sum_{i=1}^{t-1} Z_{im} \right) \left(\sum_{i=1}^{t-1} Z_{in} \right)$$

where

$\hat{p}_{uv}$ = the phenotypic correlation between m and n on the normal scale

$\hat{p}_{mn}$ = the phenotypic correlation between m and n estimated on the discrete scale

$\hat{\sigma}^2_n$ = calculated in the same manner as $\hat{\sigma}^2_m$

All other terms have been previously defined.

RESULTS AND DISCUSSION

Means and Standard Deviations

Although among the simplest descriptive statistics, means and standard deviations can be very useful in characterizing population parameters. Means and standard deviations were calculated for the initial data and are compared to the results of Aitchison (1971) in Table 8. Means and standard deviations for the three edited subsets are listed in Table 9. Most means and standard deviations vary little from those reported by Aitchison (1971). The mean score for basic form, however, increased by .22, while its standard deviation declined by .22. Thus, the cattle in the present data set were scored as thicker animals with less variation in scoring compared to the 1971 data. Other changes were in the mean for front which decreased by .20, the means for feet and legs were .15 and .16 lower than the mean for the old combined score for feet and legs, the mean for fore udder dropped by .18 and the mean for center support increased by .18. These changes indicate that cows were scored more desirable on front, feet, legs and fore udder and less desirable on center support. The unadjusted phenotypic means in Table 8 also indicate that evaluators feel cattle are most deficient in rump (3.13) and most desirable in body capacity (2.59).

Table 9 shows standard deviations for the dry cow and milk cow data subsets are approximately equivalent while those for the heifer data subset are generally smaller. Trait means vary from subset to subset with no general pattern discernible. However, dry cows are on the average thicker

Table 8. Trait overall means and standard deviations

	Means		Standard Deviations	
Trait	Present	Aitchison	Present	Aitchison
Basic Form	3.22	3.00	.74	.96
Scale	2.89	2.81	.86	.86
Front	2.73	2.93	.84	.80
Body	2.59	2.52	.78	.76
Back	2.71	2.79	.88	.89
Legs	3.00	3.15[1]	.90	.89[1]
Feet	2.99		.78	
Rump	3.13	3.11	.88	.86
Rear Udder	2.92	3.01	.86	.86
Fore Udder	2.95	3.13	.85	.81
Center	2.87	2.69	.72	.76
Teats	2.95	-	.84	-

[1]Values are for a combined feet and legs score.

Table 9. Trait means and standard deviations of the edited data for each subset

	Means			Standard deviations		
	Heifer	Dry	Milk	Heifer	Dry	Milk
Basic Form	3.28	3.43	3.18	.63	.69	.74
Scale	2.91	2.80	2.84	.76	.86	.86
Front	2.65	2.56	2.74	.74	.85	.86
Body	2.47	2.32	2.62	.75	.77	.76
Back	2.85	2.76	2.68	.84	.93	.88
Legs	2.74	2.97	2.90	.83	.90	.89
Feet	2.81	2.90	2.88	.68	.72	.73
Rump	3.15	2.99	3.12	.78	.88	.89
Fore Udder	-	2.77	2.88	-	.80	.86
Rear Udder	-	2.65	2.86	-	.82	.86
Center	-	2.67	2.62	-	.76	.77
Teats	-	2.92	2.86	-	.88	.85

[1]Values are for a combined feet and legs score.

than milk cows. Because dry cows generally carry more flesh than milk cows this result suggests that the amount of flesh has some influence on the evaluation of basic form, fatter cows being scored thicker. Dry cows also have more desirable fore and rear udder scores as compared to milk cows. The involuted udder of the dry cow may mask certain defects and, thus, result in more desirable scores. Means and standard deviations of subscores have little practical interpretation because of the nonlinear nature of subscores. Therefore, these statistics are not presented.

Subscore Analysis

Subscores are used when a trait has been scored four or five to describe the nature of the fault which resulted in an undesirable classification. Subscore frequencies broken down under trait scores four and five are listed in Table 10 for the seven traits with subscores.

Results show that often one or a few faults were responsible for most of the undesirable scores. Adding the two columns labeled overall percent in Table 10 for each subscore yields the frequency of the subscore. Front does not have an exceptionally large or exceptionally small frequency for any subscore. For feet, subscore "shallow heel" accounts for 59.03 percent (54.83 + 4.20) of the total subscores while "spread toes" accounts for less than 6 percent of the total. Other subscores with a high frequency are "too much set" and "hocks in" for legs, "sloping" and "ridgy" for rump, "bulgy and loose" for fore udder and "wide front teats" for teats. Faults with a very small (less than 1 percent) incidence are "too shallow-tilted" for rear udder and "toes out in front" for legs.

Table 10. Percentage distribution of subscores under fours and fives

Trait: Front									
	Score = 4				Score = 5				
Subscore	Number	Overall[1] Percent	Column[2] Percent	Row[3] Percent	Number	Overall Percent	Column Percent	Row Percent	Row Total
Low Front	761	27.92	30.15	90.48	80	2.93	39.60	9.51	841
Wing Shoulders	496	18.20	19.65	90.18	54	1.98	26.73	9.82	550
Narrow Front	569	20.87	22.54	93.59	39	1.43	19.31	6.41	608
Weak Crops	369	13.54	14.62	94.37	22	0.81	10.89	5.63	391
Coarse	329	12.07	13.03	97.92	7	0.26	3.47	2.08	336
Column Total	2524				202				2726

[1]Percent of the total subscore listed in the lower right corner of table.

[2]Percent of subscores under trait breakdown listed in lower left corner.

[3]Percent of a certian subscore under trait breakdown, percentages sum to 100 for each row.

Table 10. Continued

	Trait: Fore Udder								
	Score = 4				Score = 5				
Subscore	Number	Overall Percent	Column Percent	Row Percent	Number	Overall Percent	Column Percent	Row Percent	Row Total
Weak Attachment	284	7.69	8.55	91.61	26	0.70	7.03	8.39	310
Bulgy and Loose	1519	41.13	45.71	90.20	165	4.47	44.59	9.80	1684
Too Deep-Tilted	414	11.21	12.46	92.41	34	0.92	9.19	7.59	448
Too Shallow-Tilted	218	5.90	6.56	82.26	47	1.27	12.70	17.74	265
Too Short	888	24.05	26.72	90.06	98	2.65	26.49	9.94	986
Column Total	3323				370				3693

Table 10. Continued

Trait: Rump

Subscore	Score = 4 Number	Overall Percent	Column Percent	Row Percent	Score = 5 Number	Overall Percent	Column Percent	Row Percent	Row Total
High Tail Head	708	13.05	14.93	86.45	111	2.05	16.30	13.55	819
Sloping	1967	36.26	41.47	84.17	370	6.82	54.33	15.83	2337
Ridgy	1531	28.23	32.28	92.68	121	2.23	17.77	7.32	1652
Narrow	537	9.90	11.32	87.18	79	1.46	11.60	12.82	616
Column Total	4543				681				5224

Table 10. Continued

	Trait: Rear Udder								
	Score = 4				Score = 5				
Subscore	Number	Overall Percent	Column Percent	Row Percent	Number	Overall Percent	Column Percent	Row Percent	Row Total
Low Attachment	1002	27.27	30.15	88.83	126	3.43	35.90	11.17	1128
Narrow Attachment	1079	29.37	32.47	93.66	73	1.99	20.80	6.34	1152
Uneven Curvature	607	16.52	18.27	94.25	37	1.01	10.54	5.75	644
Too Deep-Tilted	615	16.74	18.51	84.36	114	3.10	32.48	15.64	729
Too Shallow-Tilted	20	0.54	0.60	95.24	1	0.03	0.28	4.76	21
Column Total	3323				351				3674

Table 10. Continued

Trait: Legs									
	Score = 4				Score = 5				
Subscore	Number	Overall Percent	Column Percent	Row Percent	Number	Overall Percent	Column Percent	Row Percent	Row Total
Too Straight	362	7.38	8.11	88.51	47	0.96	10.56	11.49	409
Too Much Set	1464	29.83	32.80	89.54	171	3.48	38.43	10.46	1635
Hocks In	2074	42.46	46.47	95.05	108	2.20	24.27	4.95	2182
Stance	537	10.94	12.03	81.86	119	2.42	26.74	18.14	656
Toes Out In Front	26	0.53	0.58	100.00	0	0.0	0.0	0.0	26
Column Total	4463				445				4908

Table 10. Continued

	Trait: Feet								
	Score = 4				Score = 5				
Subscore	Number	Overall Percent	Column Percent	Row Percent	Number	Overall Percent	Column Percent	Row Percent	Row Total
Shallow Heel	1866	54.83	63.51	92.88	143	4.2	30.75	7.12	2009
Spread Toes	179	5.26	6.09	93.23	13	0.38	2.80	6.77	192
Faulty Pasterns	674	19.81	22.94	82.10	147	4.32	31.61	17.9	821
Toes Curl	219	6.44	7.45	57.48	162	4.76	34.84	42.52	381
Column Total	2938				465				3403

Table 10. Continued

Trait: Teats

Subscore	Score = 4 Number	Overall Percent	Column Percent	Row Percent	Score = 5 Number	Overall Percent	Column Percent	Row Percent	Row Total
Wide Front Teats	1500	43.35	50.61	91.19	145	4.19	29.23	8.81	1645
Too Long or Large	453	13.09	15.28	76.91	136	3.93	27.42	23.09	589
Poorly Shaped	329	9.51	11.10	84.58	60	1.73	12.10	15.42	389
Back Too Far	72	2.08	2.43	92.31	6	0.17	1.21	7.69	78
Too Close on Side	274	7.92	9.24	86.71	42	1.21	8.47	13.29	316
Teats Strut	336	9.71	11.34	75.85	107	3.09	21.57	24.15	443
Column Total	2964				496				3460

The question arises, are certain faults considered more severe than other, thus resulting in a higher percentage of fives than would be expected? One approach to answering this question is to compare the distribution of subscores under trait scores four and five. The marginal totals from Table 10 were used to generate expected frequencies for each cell of a two-way contingency table. The expected value was then subtracted from the observed, the result squared and then divided by the expected value to yield a chi-square for each cell. The cell chi-squares were then summed over all cells yielding a table chi-square value which was used to test for independence. A significant chi-square indicates the subscore distribution is not independent of the trait score and thus some faults are considered more severe than others.

Table 11 shows that the hypothesis of independence can be rejected at the .0003 or smaller level in all cases. The addition of the two cell chi-square values for any one trait, i.e., the value under trait score four plus the value under trait score five, indicates the magnitude of the difference between observed and expected. The larger the sum, the greater the deviation from the expected value. Comparing the observed and expected frequencies indicates whether a fault is relatively more or less severe; more fours and less fives than expected indicating a less severe fault. Thus, a very large sum of chi-squares with more fives than expected indicates a very severe fault, while a small sum of chi-squares with more fives than expected would not be classified very severe as the observed distribution approximates the expected.

Table 11. Cell observed, expected and chi-square contribution of the subscore data

Trait: Front

Subscore	Score =4 Obs	Expct	Chi-Square	Score = 5 Obs	Expct	Chi-Square
Low Front	761	778.7	0.4	80	62.3	5.0
Wing Shoulders	496	509.2	0.3	54	40.8	4.3
Narrow Front	569	562.9	0.1	39	45.1	0.8
Weak Crops	369	362.0	0.1	22	29.0	1.7
Coarse	329	311.1	1.0	7	24.9	12.9

Table chi-square = 26.6 with 4 D.F.
Probability of greater value = 0.0001

Trait: Feet

Subscore	Score =4 Obs	Expct	Chi-Square	Score = 5 Obs	Expct	Chi-Square
Shallow Heel	1866	1734.5	10.0	143	274.5	63.0
Spread Toes	179	165.8	1.1	13	26.2	6.7
Faulty Pasterns	674	708.8	1.7	147	112.2	10.8
Toes Curl	219	328.9	36.7	162	52.1	232.2

Table chi-square = 362.1 with 3 D.F.
Probability of greater value = 0.0001

Table 11. Continued

Trait: Legs

Subscore	Score =4 Obs	Expct	Chi-Square	Score = 5 Obs	Expct	Chi-Square
Too Straight	362	371.9	0.3	47	37.1	2.7
Too Much Set	1464	1486.8	0.3	171	148.2	3.5
Hocks In	2074	1984.2	4.1	108	197.8	40.8
Stance	537	596.5	5.9	119	59.5	59.6
Toes Out In Front	26	23.6	0.2	0	2.4	2.4

Table chi-square = 119.7 with 4 D.F.
Probability of greater value = 0.0001

Trait: Rump

Subscore	Score =4 Obs	Expct	Chi-Square	Score = 5 Obs	Expct	Chi-Square
High Tail Head	708	716.2	0.1	111	102.8	0.6
Sloping	1967	2043.6	2.9	370	293.4	20.0
Ridgy	1531	1444.6	5.2	121	207.4	36.0
Narrow	537	538.7	0.0	79	77.3	0.0

Table chi-square = 64.8 with 3 D.F.
Probability of greater value = 0.0001

Table 11. Continued

Trait: Rear Udder

Subscore	Score =4 Obs	Expct	Chi-Square	Score = 5 Obs	Expct	Chi-Square
Low Attachment	1002	1020.2	0.3	126	107.8	3.1
Narrow Attachment	1079	1041.9	1.3	73	110.1	12.5
Uneven Curvature	607	582.5	1.0	37	61.5	9.8
Too Deep-Tilted	615	659.4	3.0	114	69.6	28.2
Too Shallow-Tilted	20	19.0	0.1	1	2.0	0.5

Table chi-square = 59.8 with 4 D.F.
Probability of greater value = 0.0001

Trait: Fore Udder

Subscore	Score =4 Obs	Expct	Chi-Square	Score = 5 Obs	Expct	Chi-Square
Weak Attachment	284	278.9	0.1	26	31.1	0.8
Bulgy and Loose	1519	1515.3	0.0	165	168.7	0.1
Too Deep-Tilted	414	403.1	0.3	34	44.9	2.6
Too Shallow-Tilted	218	238.4	1.8	47	26.6	15.8
Too Short	888	887.2	0.0	98	98.8	0.0

Table chi-square = 21.4 with 4 D.F.
Probability of greater value = 0.0003

Table 11. Continued

	Trait: Teats					
	Score =4			Score = 5		
Subscore	Obs	Expct	Chi-Square	Obs	Expct	Chi-Square
Wide Front Teats	1500	1409.2	5.9	145	235.8	35.0
Too Long or Large	453	504.6	5.3	136	84.4	31.5
Poorly Shaped	329	333.2	0.1	60	55.8	0.3
Back Too Far	72	66.8	0.4	6	11.2	2.4
Too Close on Side	274	270.7	0.0	42	45.3	0.2
Teats Strut	336	379.5	5.0	107	63.5	29.8

Table chi-square = 115.8 with 5 D.F.
Probability of greater value = 0.0001

An example of a very severe fault is "toes curl" for feet. The summed chi-square value of 268.9 (232.2 + 36.7) is very large compared to other values, i.e., "faulty pasterns" has a chi-square value of 12.5 (1.7 + 10.8). This large value for "toes curl" indicates the observed frequencies are radically different from the expected frequencies. The larger observed than expected (162 observed versus 52.1 expected) frequency of the subscore under breakdown five indicates a relatively more severe fault.

For front, relatively more severe faults are "low front" and "wing shoulders" while "narrow front," "weak crops" and "coarse" are less severe faults. Severe faults for feet are "faulty pasterns" and "toes curl"; "spread toes" and "shallow heel" are less severe faults.

Only two of the five subscores for legs have observed frequencies which vary greatly from their expected value. "Stance" is the more severe fault while "hocks in" is less severe. Summed chi-square values for the other three faults are less than 4.0 versus 44.9 for "hocks in" and 65.5 for "stance." Thus, "too straight," "too much set" and "toes out in front" do not result in an abnormally high percentage under the hypothesis of independence of either trait score. The necessary size of the summed chi-square for the observed distribution to be considered different from the expected must be made subjectively. No degrees of freedom are available for a chi-square test on a 1 x 2 table.

For rump, "high tail head" (0.7) and "narrow" (0.0) have very small summed chi-squares. "Sloping" (summed chi-square of 22.9 and 370 observed

fives versus 293.4 expected) is more severe while "ridgy" (summed chi-square of 41.2 and 121 observed fives versus 207.4 expected) is less severe.

Rear udder has one more severe fault, "too deep-tilted," and two less severe faults, "narrow attachment" and "uneven curvature." All subscores for fore udder except "too shallow-tilted," a more severe fault, have small summed chi-square values. Last, severe faults for teats are "too long or large" and "teats strut" while "wide front teats" is a less severe fault.

Evaluator Deviations

MAP evaluators work primarily in one geographic region evaluating herds within their region. Each evaluator scores several herds but each herd is scored by only one evaluator. Thus, herds are nested within evaluators. This structure requires the absorption of evaluator effects if herd effects are removed. This type of data structure also causes any region differences to be confounded with evaluator differences. Table 12 lists evaluator deviations for each data subset.

Deviations were calculated for each trait by averaging the scores for each evaluator and then subtracting the overall trait mean from the evaluator average for the trait. Deviations were then averaged over all traits to arrive at an overall deviation for each evaluator. Again, any geographic differences are included in the deviations listed in Table 12. Thus, an evaluator working a region with superior animals should have a

Table 12. Evaluator deviations for M.A.P. data

	Evalutor number					
	1 (1446)[1]	2 (1938)	3 (2481)	4 (322)	7 (185)	Range
	Milk cow subset					
Basic Form	-.22	.13	-.01	.26	-.15	.48
Scale	.03	-.07	-.02	.07	-.01	.14
Front	-.09	-.03	-.05	-.17	.34	.51
Body	.19	.08	-.09	-.13	-.04	.32
Back	.14	.02	.18	-.18	-.14	.36
Legs	-.21	-.06	.12	-.19	.34	.55
Feet	.00	.01	.03	-.27	.22	.49
Rump	.15	-.06	.06	-.32	.15	.47
Rear Udder	.05	-.03	.04	-.20	.12	.32
Fore Udder	-.20	.05	-.07	-.04	.26	.46
Center	.02	-.10	-.11	.00	.17	.28
Teats	-.16	-.03	.09	-.02	.11	.27
Average	-.02	.00	.02	-.10	.12	.22

[1]Number of observations scored are in parentheses.

Table 12. Continued

	Evalutor number					
	1 (259)	2 (325)	3 (331)	4 (54)	7 (31)	Range
	Dry cow subset					
Basic Form	-.15	.13	-.12	.22	-.11	.37
Scale	.06	-.07	.03	.07	-.09	.15
Front	-.13	.13	-.13	-.11	.30	.43
Body	.18	.13	-.01	-.03	-.28	.46
Back	.22	.15	.30	-.27	-.42	.72
Legs	-.24	-.03	.07	-.17	.37	.61
Feet	-.04	.02	-.01	-.36	.37	.73
Rump	-.05	-.02	.21	-.28	.14	.49
Rear Udder	-.01	-.04	-.12	-.13	.30	.43
Fore Udder	-.26	.03	-.10	-.15	.50	.76
Center	-.01	-.06	-.18	-.12	.38	.56
Teats	-.16	-.03	.10	-.18	.25	.43
Average	-.05	.03	.00	-.13	.14	.27

Table 12. Continued

	Evalutor number					
	1 (236)	2 (205)	3 (145)	4 (34)	7 (10)	Range
	Heifer subset					
Basic Form	-.23	.11	-.07	.32	-.13	.55
Scale	.13	-.06	-.14	.16	-.10	.30
Front	-.08	-.05	-.08	.00	.19	.27
Body	.11	-.04	-.23	.13	.04	.36
Back	-.05	-.18	.21	-.11	.15	.39
Legs	-.37	-.09	.24	-.10	.31	.68
Feet	-.15	-.07	.04	-.02	.20	.35
Rump	.04	-.15	.03	-.25	.34	.59
Average	-.08	-.07	.00	.02	.13	.21

negative deviation. Such differences can not be estimated without inter-regional scoring by each evaluator.

For the milk cow subset, the largest evaluator deviation range for a single trait is -.21 to .34 for legs, while the smallest range is -.07 to .07 for scale. A deviation range of .55 on a scale of 1 to 5 is fairly large. Other ranges are listed in Table 12. Overall evaluator deviations ranged from -.10 to .12. Results show that deviations for the principle evaluators (numbers 1, 2, and 3) are small or zero; -.02, .00 and .02, respectively. Evaluator 4 shows an overall deviation of -.10 while evaluator 7 shows an overall deviation of .12. The area covered by the principle evaluators was much larger, thus deviations are less likely to be affected by geographic differences or chance differences in the herds scored. The small overall deviations of the principle evaluators support this hypothesis.

The dry cow and heifer subsets show larger deviation ranges compared to the milk cow subset. The smaller sample size of the two subsets at least partially explains this difference. The ranking of evaluators for a single trait is generally consistent across subsets. Overall deviations for the dry cow subset show the principle evaluators to be again grouped around zero deviation, evaluator 4 to again show a larger negative deviation and evaluator 7 to again show a larger positive deviation. Overall deviations for the heifer subset show a different pattern. Evaluator 7 again shows a large positive deviation and evaluator 3 a zero deviation. Evaluators 1 and 2, however, show the largest negative deviations in contrast to their small deviation in the other subsets and evaluator 4 shows

a small positive deviation in contrast to the large negative deviation in the other subsets.

Least Squares Analysis of Variance

After the absorption of herd and evaluator effects, the models presented in the previous section were applied to each data subset. The analysis procedure was programmed by the author for all subsets. The heifer subset was also analyzed using Walter Harvey's LSMLGP program for verification. The least squares analysis of variance for the three data subsets is presented in Table 13.

Parity effects

F ratios from the least squares analysis of variance show that parity effects are significant at the .01 level for scale, front, body, rump, rear udder, fore udder and teats, but were nonsignificant at .05 level for basic form, back, legs, feet and center support. However, all traits show a nonsignificant parity effect in the dry cow subset. This result implies that dry cow records should not be adjusted for parity effects.

Analysis procedures also produced least squares constant estimates ($\hat{\beta}$'s) for parity classifications. Estimates for the milk cow subset are presented in Table 14. The udder traits; rear udder, fore udder, center support and teats, have negative constant estimates for parities one and two and positive estimates for all greater classifications. Thus, first and second parity animals receive more desirable scores (closer to one) than older animals. This result reflects the deterioration of the udder

Table 13. Least squares within herd analysis of variance for M.A.P. traits

Milk Cow Subset		Basic Form		Scale	
	df.	M.S.	F	M.S.	F
Parity	4	0.57	1.03	4.59	7.73**
Eval. * Par.	16	0.75	1.36	1.78	2.99**
Sire	101	8.11	14.66**	6.46	10.88**
Lin. Days Milk	1	0.41		8.75	
Quad. days Milk	1	1.83	3.31	2.28	3.84*
Error	5894	0.55		0.59	
		Front		Body	
	df.	M.S.	F	M.S.	F
Parity	4	2.34	3.76**	10.58	23.44**
Eval. * Par.	16	1.20	1.93*	1.38	3.06**
Sire	101	3.99	6.42**	4.35	9.65**
Lin. Days Milk	1	2.48		5.16	
Quad. Days Milk	1	0.90	1.45	0.01	0.02
Error	5894	0.62		0.45	

* Significant at the .05 level.

** Significant at the .01 level.

Table 13. Continued

Milk Cow Subset		Back		Legs	
	df.	M.S.	F	M.S.	F
Parity	4	0.81	1.17	1.29	1.84
Eval. * Par.	16	1.58	2.29**	1.39	1.98**
Sire	101	1.83	2.65**	2.53	3.59**
Lin. Days Milk	1	19.53		14.10	
Quad. Days Milk	1	10.87	15.78**	8.41	11.93**
Error	5894	0.69		0.70	
		Feet		Rump	
	df.	M.S.	F	M.S.	F
Parity	4	0.91	1.92	8.51	12.05**
Eval. * Par.	16	0.98	2.09**	2.13	3.01**
Sire	101	1.68	3.56**	1.92	2.72**
Lin. Days Milk	1	5.20		0.63	
Quad. Days Milk	1	3.41	7.23**	1.09	1.54
Error	5894	0.47		0.72	

Table 13. Continued

Milk Cow Subset		Rear Udder		Fore Udder	
	df.	M.S.	F	M.S.	F
Parity	4	7.66	12.15**	7.30	11.49**
Eval. * Par.	16	1.58	2.50**	5.67	8.92**
Sire	101	1.81	2.87**	1.50	2.36**
Lin. Days Milk	1	44.07		3.70	
Quad. Days Milk	1	36.97	58.66**	7.95	12.51**
Error	5894	0.63		0.64	
		Center		Teats	
	df.	M.S.	F	M.S.	F
Parity	4	1.04	1.99	5.49	8.48**
Eval. * Par.	16	0.64	1.22	4.04	6.25**
Sire	101	1.44	2.74**	2.35	3.63**
Lin. Days Milk	1	10.24		5.80	
Quad. Days Milk	1	5.24	9.80**	2.45	3.79*
Error	5894	0.53		0.61	

Table 13. Continued

Dry Cow Subset		Basic Form		Scale	
	df.	M.S.	F	M.S.	F
Parity	4	0.38	1.07	0.29	0.49
Eval. * Par.	16	0.24	0.68	1.24	2.05**
Sire	47	1.61	4.48**	1.70	2.82**
Error	666	0.35		0.60	
		Front		Body	
	df.	M.S.	F	M.S.	F
Parity	4	0.76	1.26	0.42	0.86
Eval. * Par.	16	0.62	1.03	0.87	1.78*
Sire	47	1.13	1.86**	1.69	3.45**
Error	666	0.61		0.49	
		Back		Legs	
	df.	M.S.	F	M.S.	F
Parity	4	0.57	0.75	0.13	0.18
Eval. * Par.	16	0.46	0.61	0.67	0.96
Sire	47	1.34	1.77**	1.67	2.39**
Error	666	0.75		0.70	

Table 13. Continued

Dry Cow Subset		Feet		Rump	
	df.	M.S.	F	M.S.	F
Parity	4	0.11	0.24	1.12	1.59
Eval. * Par.	16	0.60	1.21	0.93	1.32
Sire	47	0.71	1.61**	0.80	1.13
Error	666	0.47		0.71	
		Rear Udder		Fore Udder	
	df.	M.S.	F	M.S.	F
Parity	4	0.72	1.28	0.24	0.44
Eval. * Par.	16	1.21	2.14**	0.59	1.07
Sire	47	1.24	2.21**	0.92	1.68**
Error	666	0.56		0.55	
		Center		Teats	
	df.	M.S.	F	M.S.	F
Parity	4	0.13	0.23	0.61	0.94
Eval. * Par.	16	0.38	0.71	1.03	1.59
Sire	47	0.84	1.55**	1.60	2.48**
Error	666	0.54		0.65	

Table 13. Continued

Heifer Subset	df.	Basic Form M.S.	Basic Form F	Scale M.S.	Scale F	Front M.S.	Front F
Sire	30	1.40	4.86**	1.27	3.13**	1.10	2.58**
Error	382	0.29		0.41		0.42	

	df.	Body M.S.	Body F	Back M.S.	Back F	Feet M.S.	Feet F
Sire	30	1.34	2.95**	0.56	0.85	0.67	1.13
Error	382	0.46		0.67		0.59	

	df.	Legs M.S.	Legs F	Rump M.S.	Rump F
Sire	30	0.55	1.43**	1.08	2.00**
Error	382	0.38		0.54	

Table 14. Least squares parity constants for the milk cow subset

	Parity Number				
	1	2	3	4	5+
Basic Form	.0571	-.0134	-.0113	.0001	-.0325
Scale	.1713	-.0268	.0233	-.0936	-.0684
Front	.1282	.0040	-.0136	-.0931	-.0255
Body	.2610	.1560	-.0330	-.1085	-.2754
Back	.0088	.0633	-.0628	.0275	-.0368
Legs	.0173	-.0324	.0089	-.1300	.1361
Feet	-.0792	-.0321	-.0233	.0622	.0725
Rump	.2196	-.0529	-.0814	-.0811	-.0042
Rear Udder	-.2003	-.1350	.0549	.0054	.2750
Fore Udder	-.1950	-.1482	.0541	.0304	.2554
Center	-.1582	-.1033	.0578	.0523	.1514
Teats	-.1944	-.0994	.0328	.0900	.1710

as a cow proceeds through her productive life. Also, evaluators properly did not make subjective adjustments for udder deterioration.

All other traits except feet and legs show a positive first parity constant and a negative fifth and greater parity constant with a near random pattern for intermediate parities. Immaturity and a lack of selection for younger cattle and the required stronger confirmation for a long productive life in older cattle may explain this result. Parity estimates for feet show deteriorating confirmation over productive life while estimates for legs show no discernible pattern.

Interaction effects

All traits except basic form and center support show significant evaluator by parity interactions for the milk cow subset. In contrast, only rear udder, body and scale show significant interactions for the dry cow subset. Constant estimates obtained for interactions did not yield a practical interpretation and are not presented.

Stage of lactation effects

Two variations of the model given for the milk cow subset were analyzed because the F ratio is only a valid test for the highest degree polynomial function fit. Table 13 does not list an F value for the linear effect of days in milk for this reason. The first contained only the linear effect of days in milk. All traits showed a significant linear effect. Regression coefficients obtained from the analysis are listed in Table 15.

A second model was then analyzed which contained both linear and quadratic terms. Table 13 shows significant quadratic effects for scale,

Table 15. Regression coefficients and effect at 200 days of linear and quadratic models for days in milk

	Linear model[1]		Quadratic model[2]		
	b1	ect.[3]	b1	b2	ect.
Basic Form	.000888	.18	.000296	.000002	.14
Scale	-.000700	-.14	-.011362	.000002	-.19
Front	-.001141	-.23	-.000725	-.000001	-.11
Body	-.001084	-.22	-.001046	-.000000	-.21
Back	-.000591	-.12	-.002035	.000004	-.25
Legs	.000459	.09	.001729	-.000004	.18
Feet	.000241	.05	.001050	-.000003	.09
Rump	-.000822	-.16	-.000366	-.000001	-.11
Rear Udder	.000394	.08	.003056	-.000008	.29
Fore Udder	-.000349	-.07	.000886	-.000004	.02
Center	-.000471	-.09	-.001474	.000003	-.17
Teats	-.000423	-.09	-.001109	.000002	-.14

[1]Model using b1(days in milk).

[2]Model using b1(days in milk) + b2(days in milk)^2.

[3]Ect. is the effect of days in milk at 200 days.

back, legs, feet, rear udder, fore udder, center support and teats. Thus, the quadratic term is necessary to describe the effect of days in milk on these traits while the linear effect alone is sufficient for basic form, front, body and rump.

Regression coefficients obtained from the quadratic model are listed in Table 15. However, it is often hard to visualize this type of effect by inspection of regression coefficients. As an aid in visualization, the regression coefficients were used to plot linear and quadratic effects of days in milk over the course of a 305 day lactation (Figure 2). The linear and quadratic curves in Figure 2 both have the same intercept (the raw trait mean) because the absorption process removed the actual intercept. Thus, these graphs only reflect the form of the curve. The linear and quadratic lines may not be in their proper relationship to each other because each curve may have a different intercept.

Edema of the udder, high production in early lactation and involution of the udder in late lactation may explain quadratic effects exhibited by the udder traits. The edema could cause the rear udder to look higher and result in better scores while causing the fore udder to look bulgy and put increased strain on center support resulting in higher scores. High production could also cause the fore udder to look bulgy. The coincidence of the peak production and peak of the quadratic effect of days in milk for fore udder support this hypothesis. Udder involution could mask faults and result in the lower score at the end of the lactation.

The excess flesh of early and late lactation may account for the quadratic effects shown by back and scale, however, the least desirable

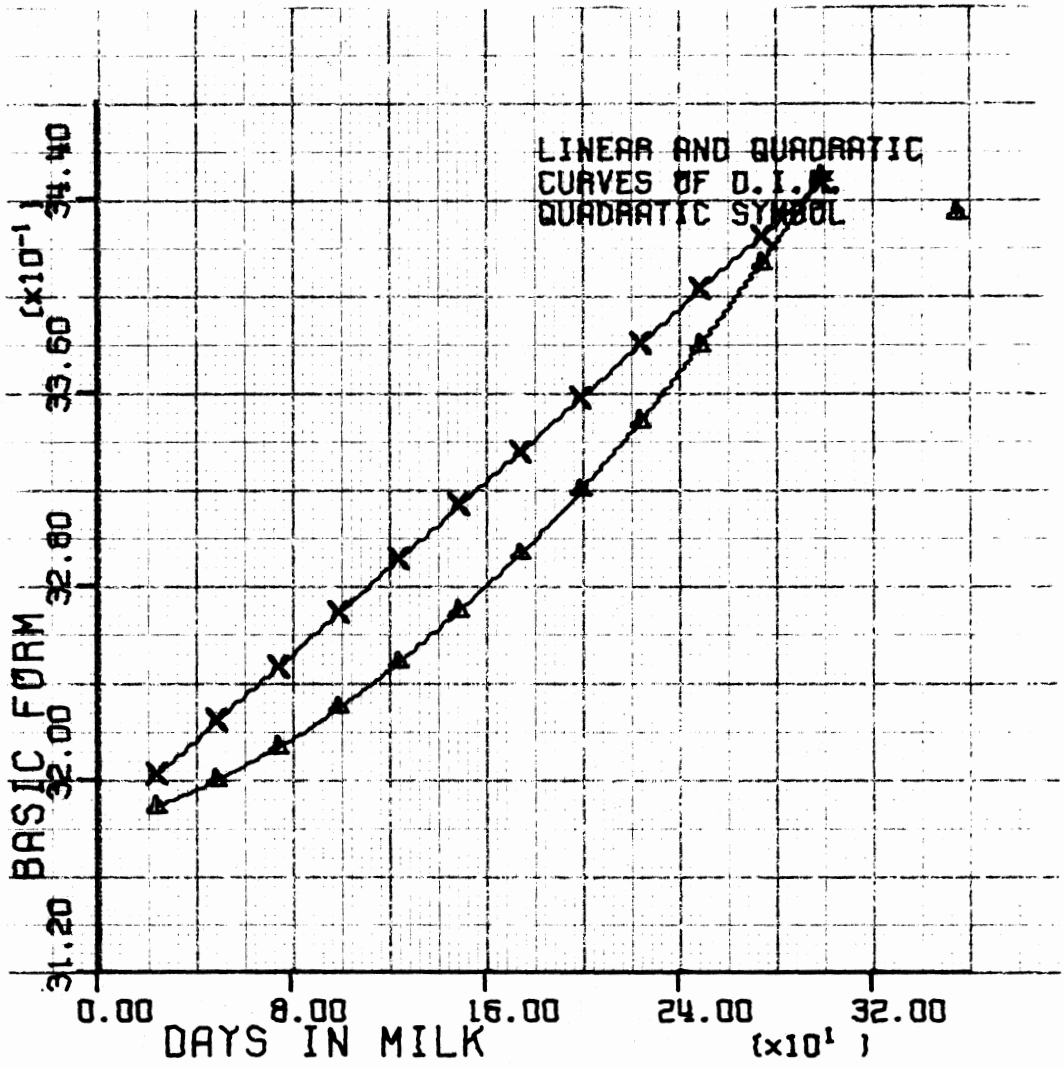

Figure 2. Linear and quadratic effects of days in milk plotted over a 305 day lactation.

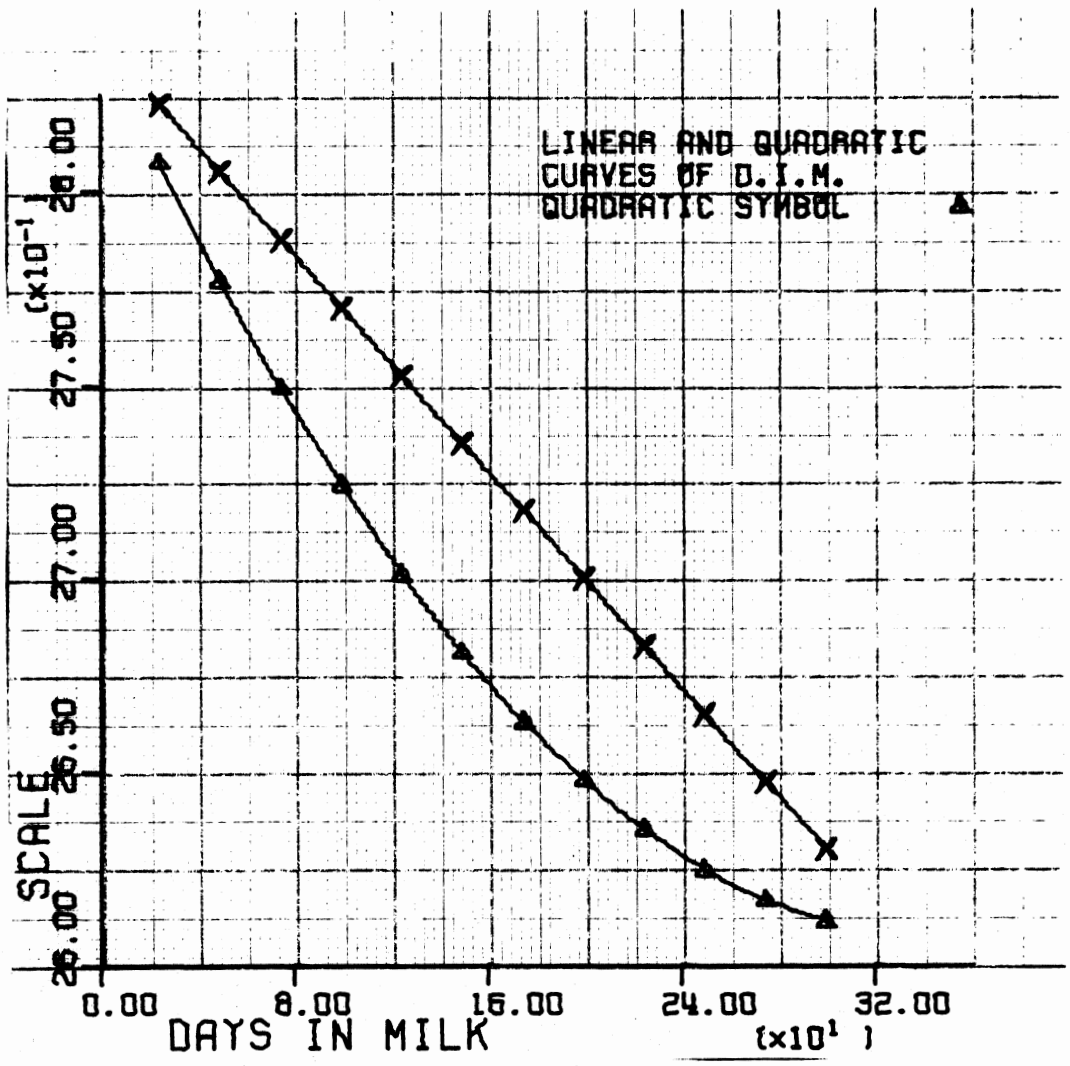

Figure 2. (Continued)

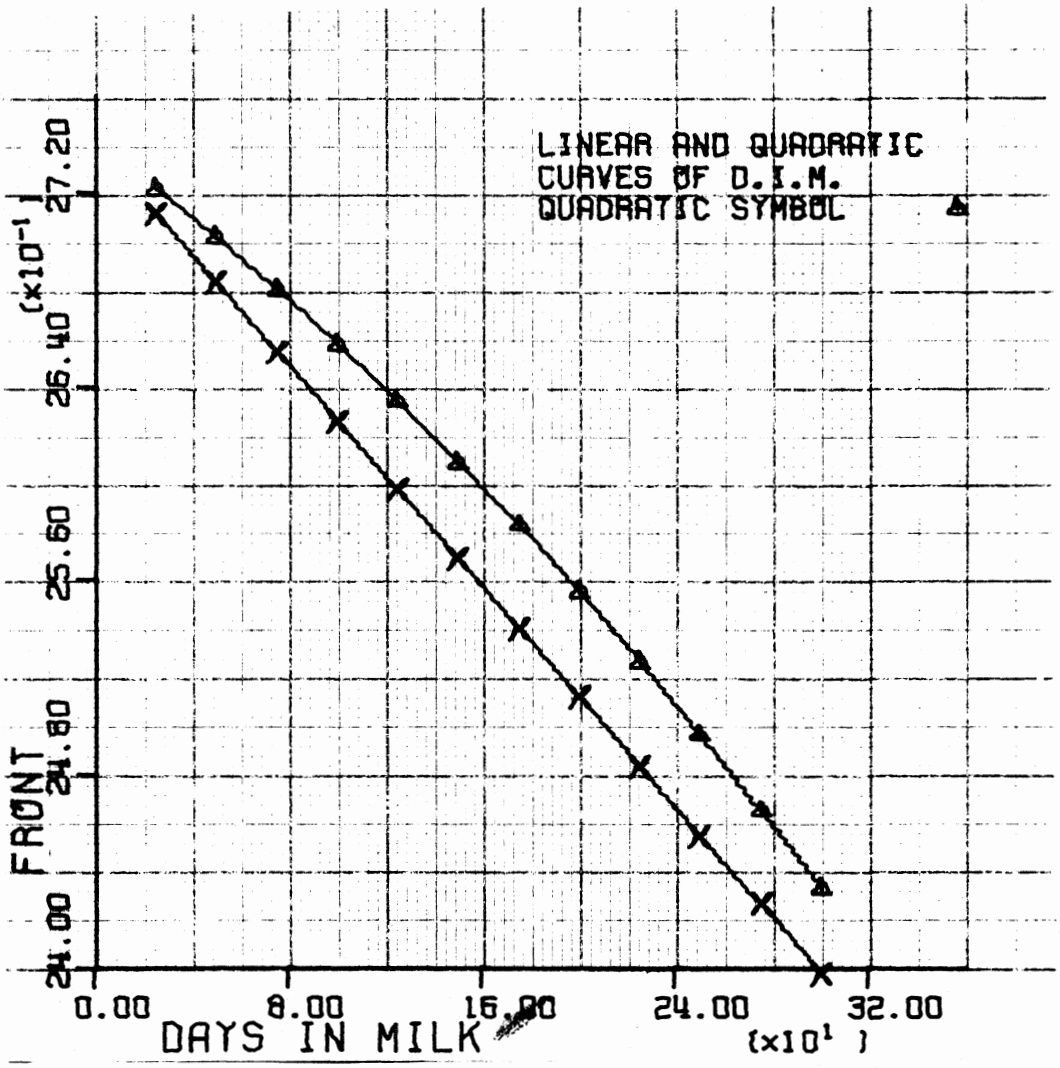

Figure 2. (Continued)

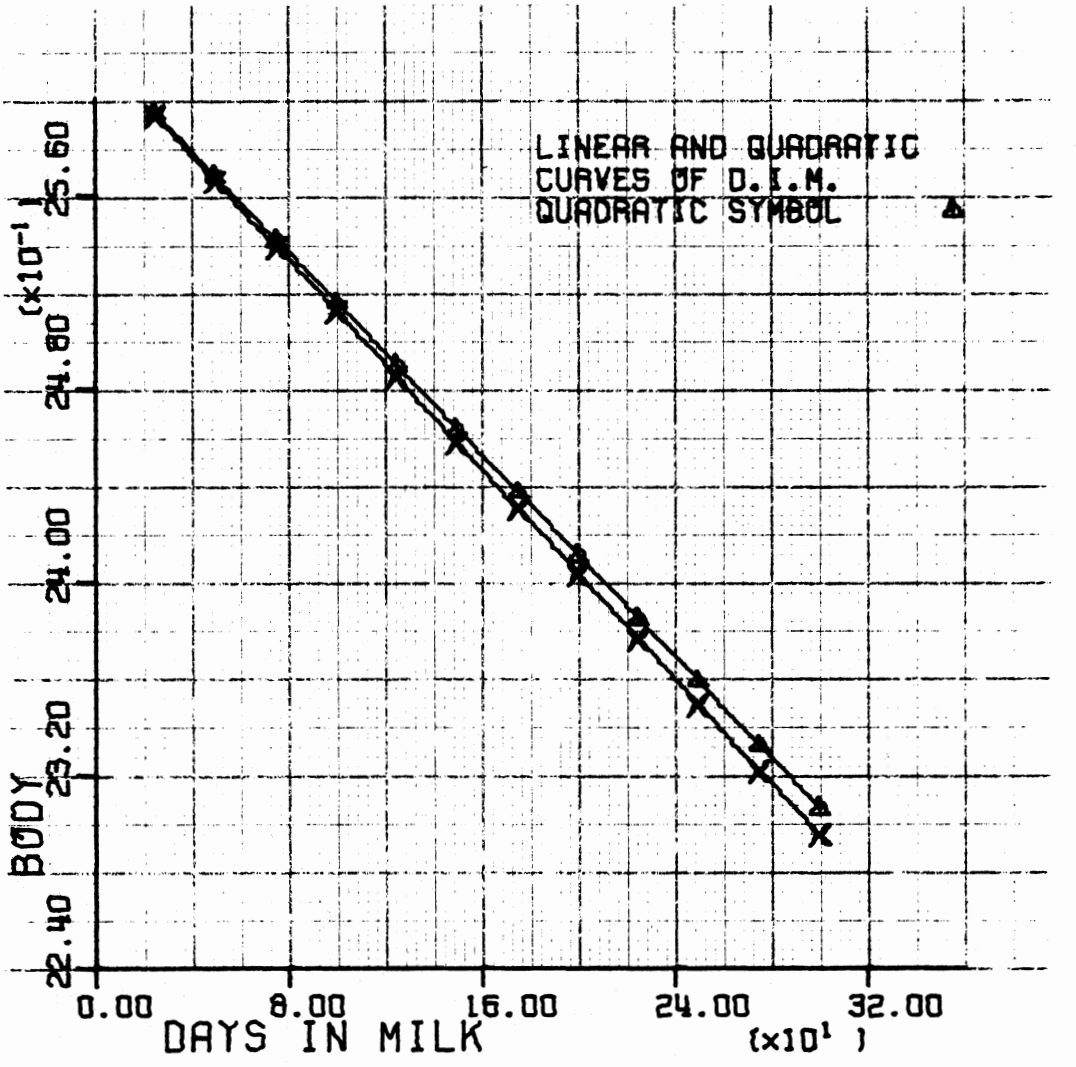

Figure 2. (Continued)

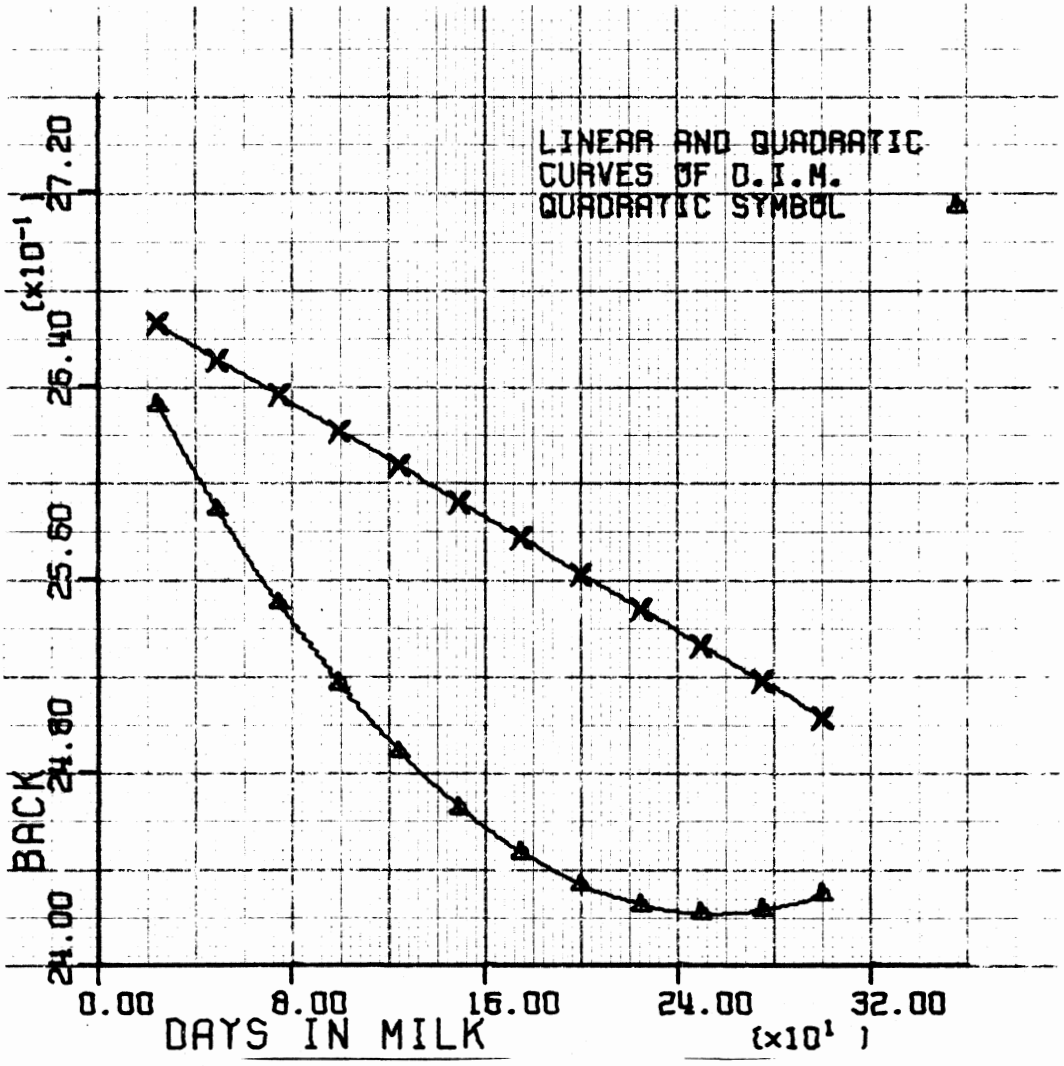

Figure 2. (Continued)

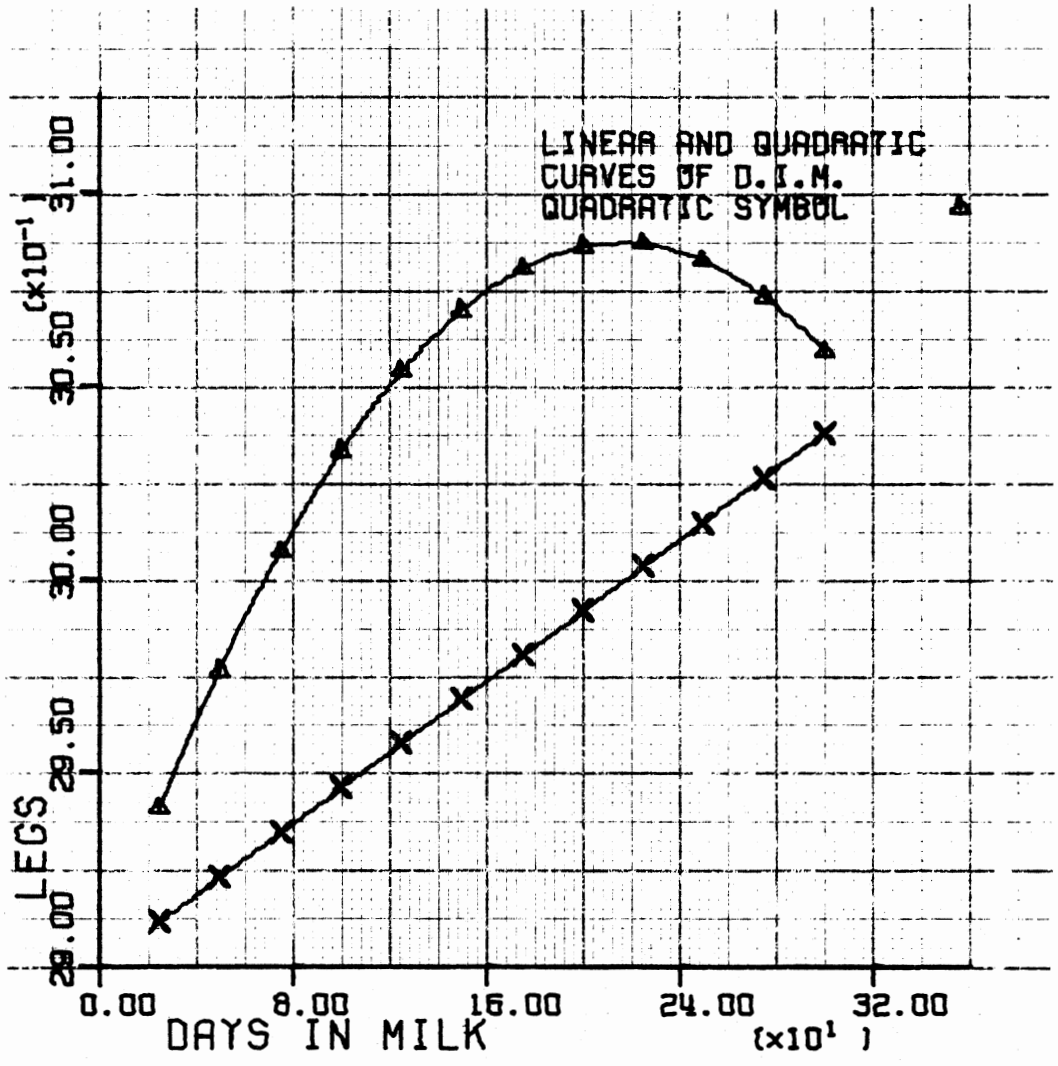

Figure 2. (Continued)

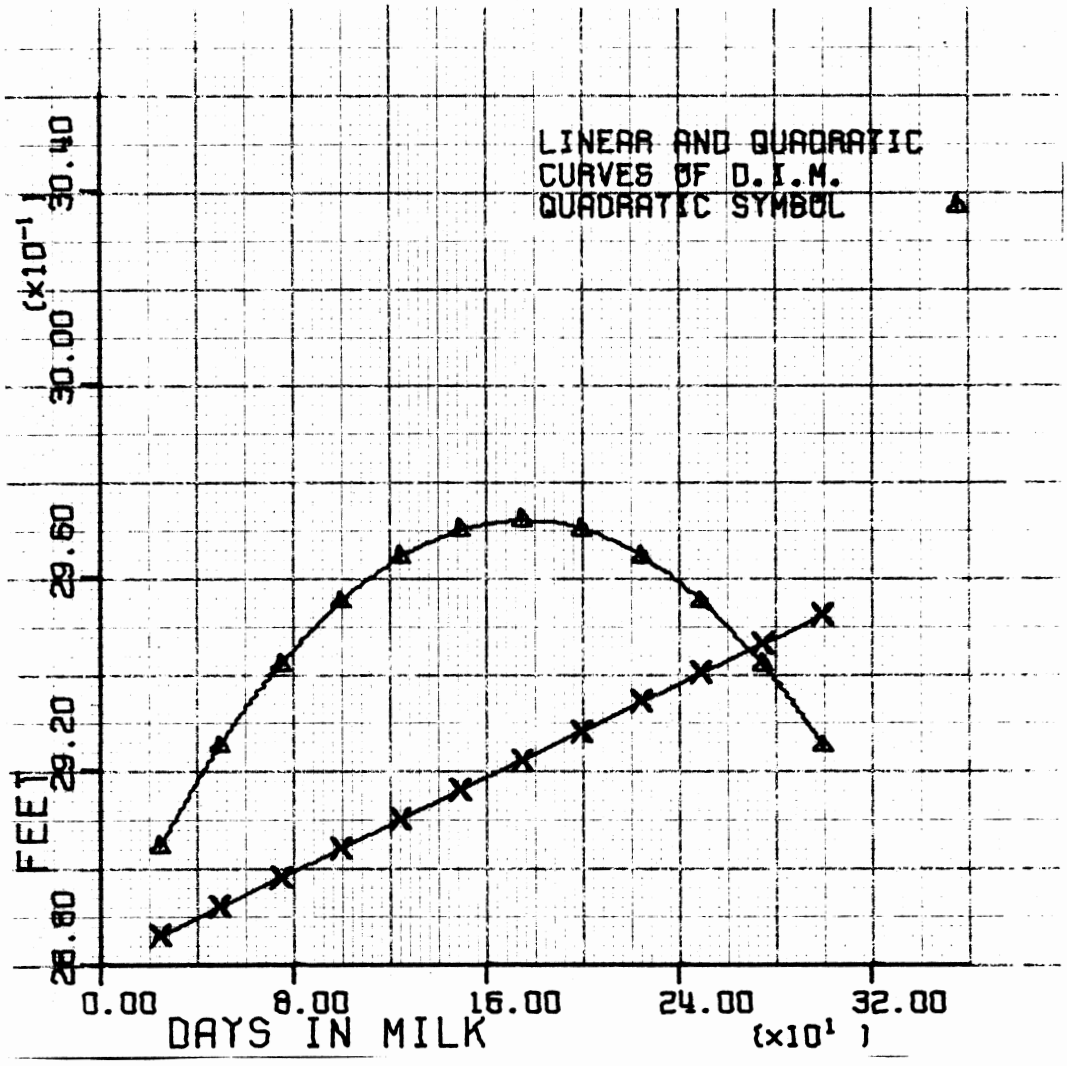

Figure 2. (Continued)

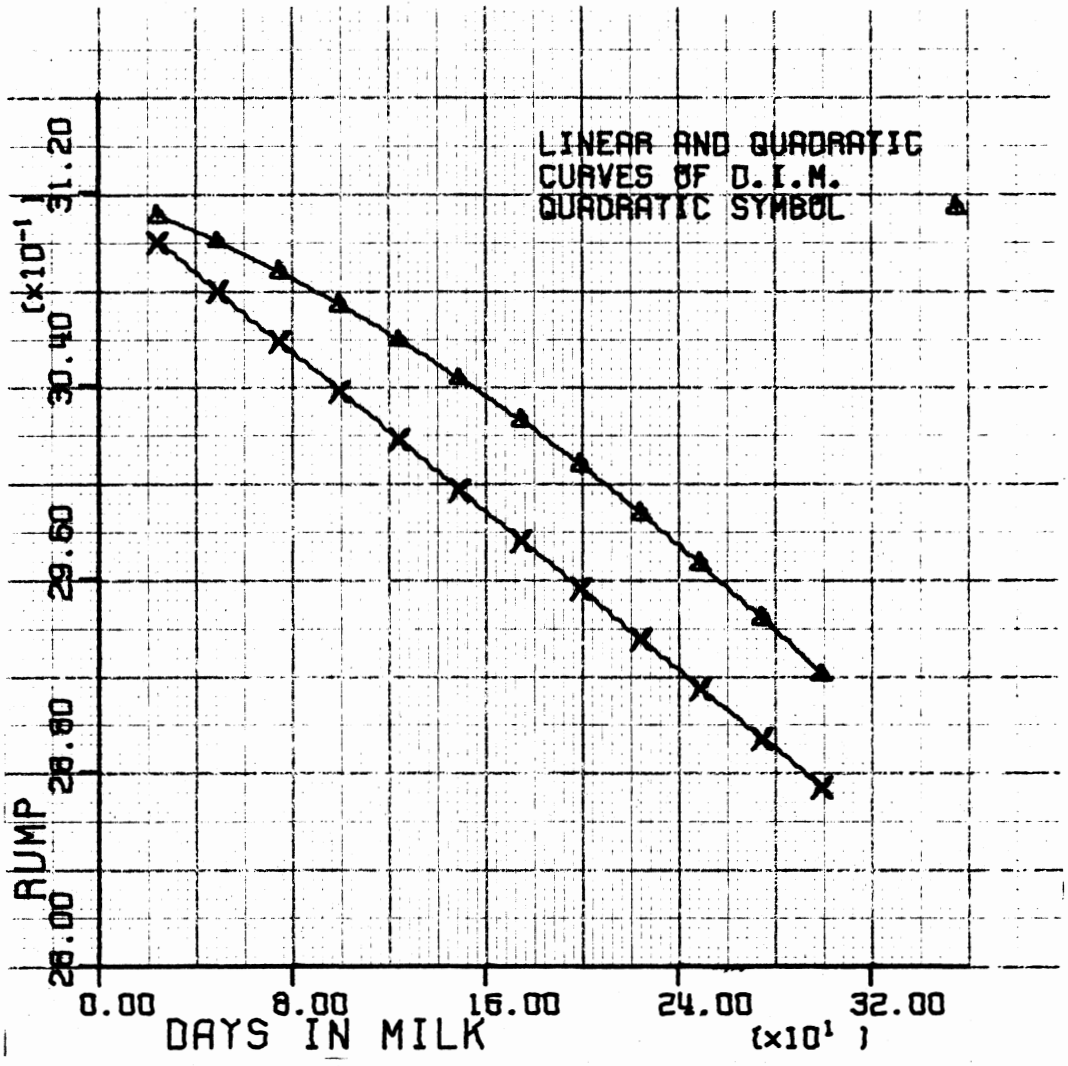

Figure 2. (Continued)

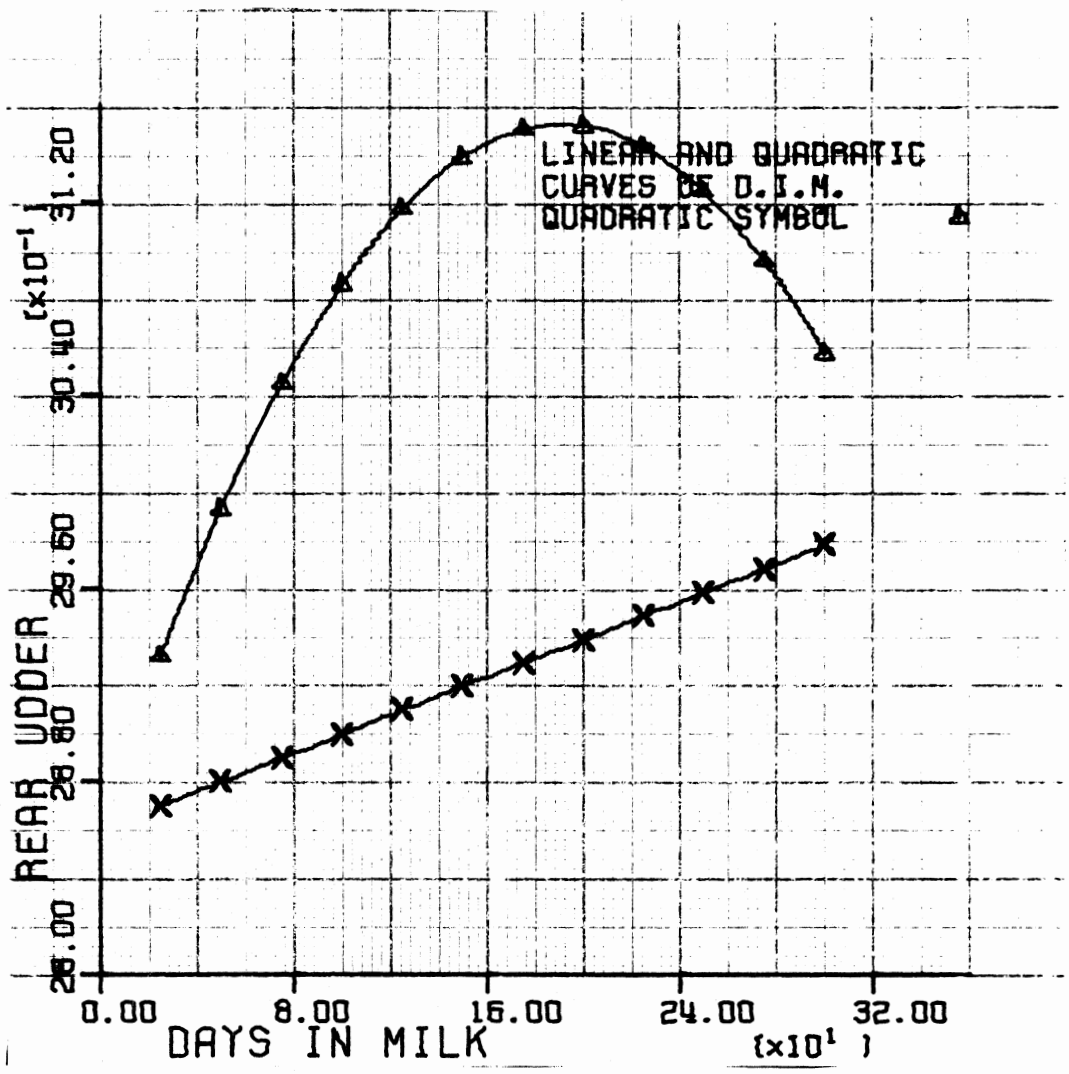

Figure 2. (Continued)

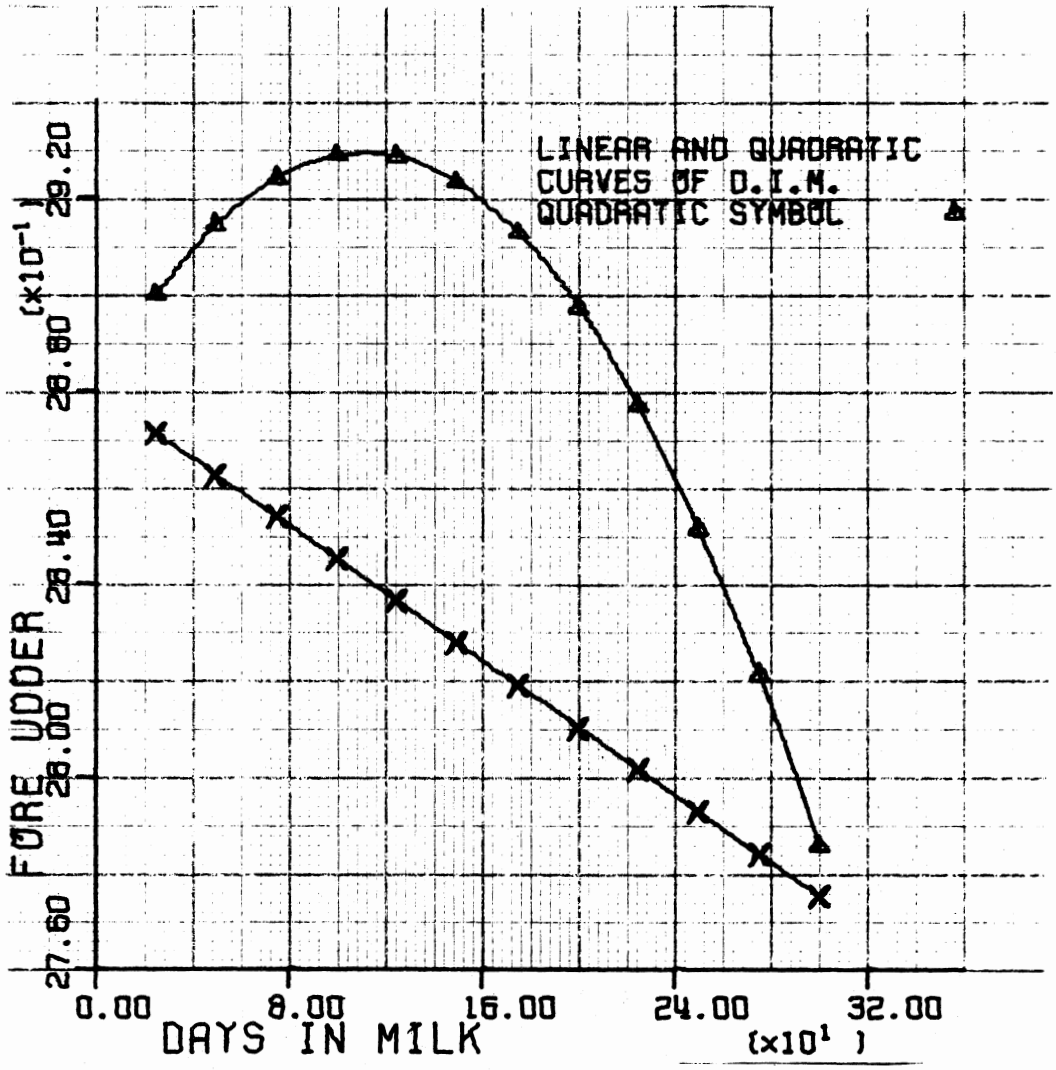

Figure 2. (Continued)

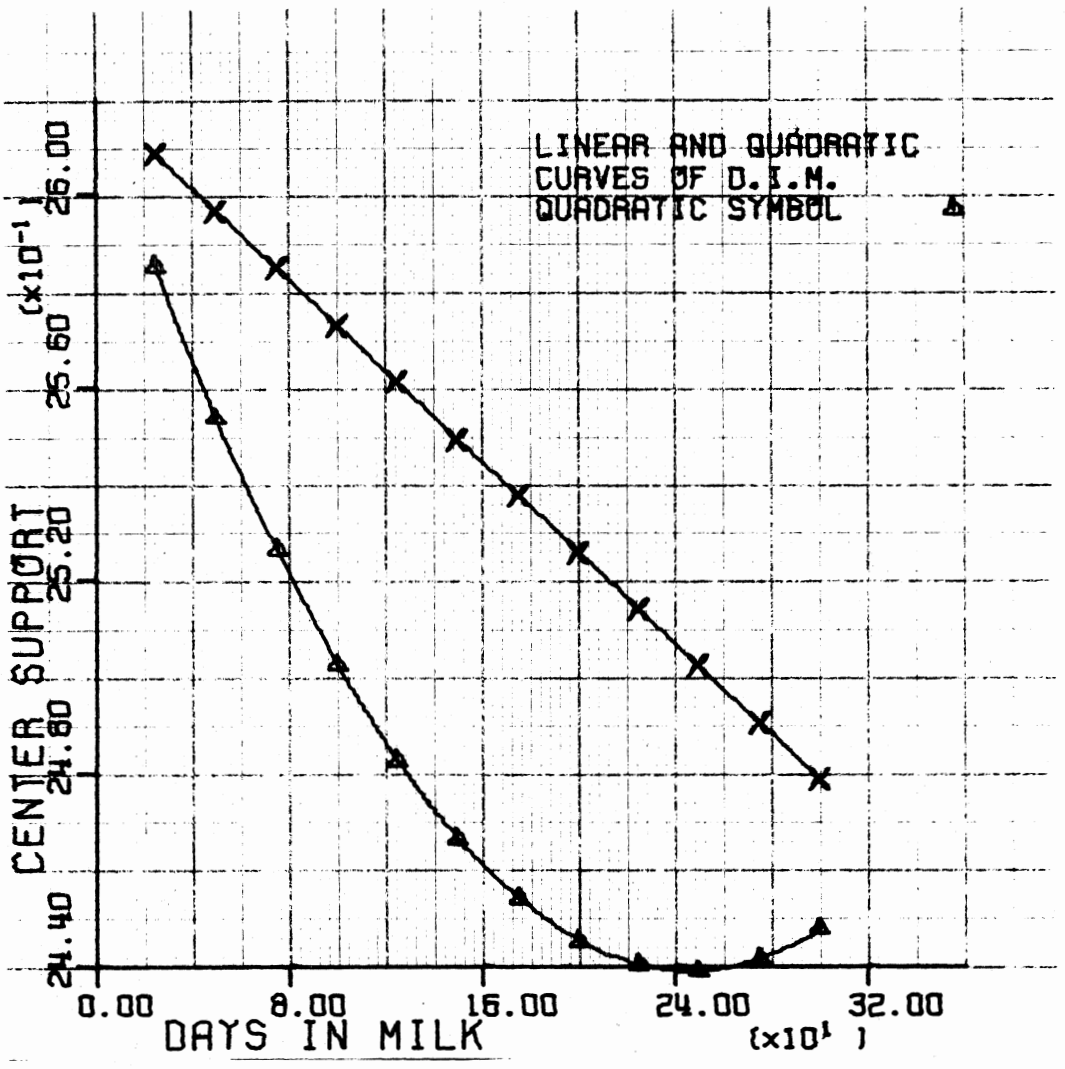

Figure 2. (Continued)

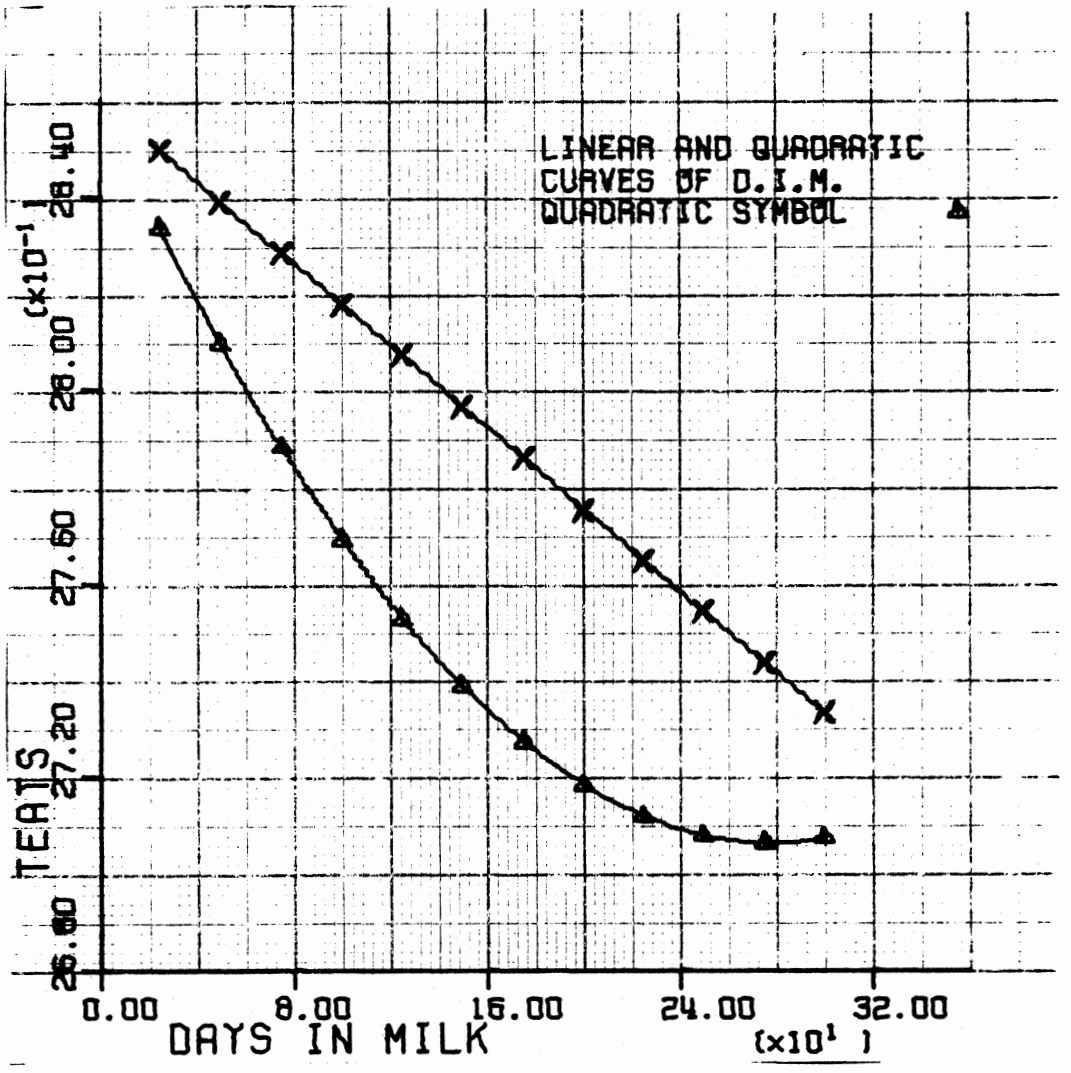

Figure 2. (Continued)

scores are found at the beginning of lactation when the animal is at or near its maximum weight. Thus, flesh is not concealing faults. Confinement of milking cows on cement could cause feet problems and higher scores in mid-lactation while pasturing of dry cows could result in more desirable feet score in early and late lactation. No explanation for the quadratic effect shown by legs is available at this time.

Another useful tool in interruptation is the cumulative effect of days in milk at a fixed point during a lactation. In other words, at any point in a lactation how much higher or lower would an animal be scored compared to zero days in milk. This technique can be applied at any point of the lactation; results at the 200 days in milk point are listed in Table 15. The .29 value for rear udder under the quadratic model indicates a cow will score .29 higher if evaluated at 200 days versus zero days.

Sire effects

Significant sire effects are shown in Table 13 for all traits in the milk cow subset, all traits except rump in the dry cow subset, and all traits except back and legs in the heifer subset. As sire differences are the basis for the heritability calculations in this analysis such results are encouraging.

Heritabilities

Heritabilities of all type components were estimated using a paternal half-sib analysis. This analysis assumes that animals with a common sire, but unrelated dams have 25 percent of their genes in common. Thus, 25 percent of the additive genetic variation is accounted for by sire differ-

ences. The sire and error components of variance obtained from the least squares analysis were used to estimate heritability using the formula: $4\hat{\sigma}_s^2/(\hat{\sigma}_s^2 + \hat{\sigma}_e^2)$. Table 16 lists heritability estimates with their standard error calculated using the methods of Swiger et al. (1964).

Heritability estimates from the milk cow subset for basic form, scale, front and body are about 50 percent larger than estimates reported by Aitchison et al. (1972). In contrast, heritability estimates for the other eight traits are about 50 percent smaller than estimates reported by Aitchison et al. (1972). The more complete model used for this study may partially account for these discrepancies.

White and Vinson (1976) used a model similar to the one used in the present study to analyze the HFAA data. A heritability estimate of .51 was reported for scale versus .60 for the present study and .39 for Aitchison et al. (1972). Although the present estimates for feet (.18) and legs (.18) are substantially less than Aitchison et al. (1972) estimate of .33 for a combined feet and legs score, White and Vinson (1976) reported estimates of .15 for feet and .14 for legs. Norman and VanVleck (1972) reported an estimate of .11 for feet and sixteen udder traits were found to have heritabilities ranging from .01 to .16. Present estimates of .13 for rear udder, .10 for fore udder, and .12 for center support are within this range. It must be remembered that MAP trait definitions do not always agree with HFAA definitions and thus heritabilities may be estimates of different characteristics although the trait names are similar.

All other studies examined have reported estimates smaller than the present .54 for body and greater than the present .12 for rump. Because

Table 16. Heritabilities, standard errors, and corrected heritabilities for the three data subsets

	Milk cows			Dry cows			Heifers		
	h[1]	S.E[2]	cor.[3]	h	S.E.	cor.	h	S.E.	cor.
Basic Form	.83	.10	.98	.81	.17	1.05	.94	.24	1.18
Scale	.60	.08	.66	.45	.13	.50	.58	.19	.83
Front	.39	.05	.39	.22	.10	.26	.47	.17	.56
Body	.54	.07	.62	.27	.10	.36	.54	.18	.63
Back	.12	.02	.13	.21	.10	.23	-.05	.07	-.06
Legs	.18	.03	.20	.35	.12	.41	.04	.09	.05
Feet	.18	.03	.21	.16	.09	.19	.13	.11	.16
Rump	.12	.02	.14	.04	.07	.05	.29	.14	.35
Rear Udder	.13	.03	.15	.33	.11	.34			
Fore Udder	.10	.02	.11	.19	.09	.20			
Center	.12	.02	.14	.15	.09	.47			
Teats	.20	.04	.22	.37	.12	.40			

[1]H is heritability.

[2]S.E. is the standard error of heritability.

[3]Cor. is the heritability estimate corrected for discontinuity.

basic form is unique to the MAP program other studies provide no basis for comparison. However, the present estimate of .83 is exceptionally large for a quantitative trait. The practice of evaluators recording the sire identification before evaluation could result in a preconceived idea of confirmation by paternal half-sib groups. Since basic form receives the major emphasis in the program, such a bias should effect its scoring to a greater extent than the scoring of other traits. One method to locate such a bias is to estimate heritability using a daughter-dam regression.

A total of 1,110 daughter-dam pairs were located with sufficient information for analysis. Prior to analysis both daughter and dam records were adjusted for the effects of parity and days in milk. This was accomplished by subtracting the least squares constant for the parity of the cow and the regression coefficients multiplied by the number of days in milk for the cow from each record. Constants and coefficients obtained from the least squares analysis were used for these adjustments. The records were considered free from the influence of parity and stage of lactation effects after adjustment.

The adjusted records were then analyzed using the model:

$$Y_{ijkl} = u + S_i + H_j + D_k + e_{ijkl}$$

where

Y_{ijkl} = record of the lth daughter with the kth dam score in the jth herd and sired by the ith sire

S_i = effect of the ith sire

H_j = effect of jth herd

D_k = record of the kth dam

e_{ijkl} = a random error component with mean zero and variance σ^2_e

Herd-sire subclasses were absorbed in the above model. This absorption will not only remove herd and sire effects but also removes the herd by sire interaction. The removal of sire effects should remove bias due to the mating program. The D_k component of the model is the effect of the dam's score on the daughter trait being analyzed. Thus, dam score is being fit as a continuous variable.

Table 17 lists the heritability estimates and their standard errors obtained from the above analyses. All estimates are considerably lower than corresponding paternal half-sib estimates and results of most other studies. However, only the paternal half-sib estimates for basic form, scale and body fall outside of a 95 percent confidence interval on the daughter-dam estimate. The reason for the large discrepancy between the half-sib and daughter-dam analyses is unknown.

Several characteristics of the MAP program, however, could influence the estimates. First, negative assortative mating could reduce the variance of daughters while selection could reduce the variance of dams. Variances of daughter and dam records were found to be approximately equal. How much, if any, effect the above factors would have on daughter-dam estimates of heritability is unknown.

Second, a cow with an undesirable rating on a trait is mated to a bull known to sire progeny with a desirable rating on the trait. Thus, a certain type of cow is often mated to a bull. This practice could reduce the within sire variance and result in an inflated estimate of herita-

Table 17. Comparison of heritabilities from daughter-dam and half-sib analyses for the milk cow subset

Trait	Daughter-Dam estimate	Half-Sib estimate
Basic Form	.12 (.16)[1]	.83 (.10)
Scale	.16 (.19)	.60 (.08)
Front	.05 (.17)	.38 (.05)
Body	.05 (.14)	.54 (.07)
Back	.00 (.16)	.12 (.02)
Legs	.04 (.16)	.18 (.03)
Feet	.00 (.14)	.18 (.03)
Rump	.04 (.15)	.12 (.02)
Rear Udder	-.14 (.15)	.13 (.03)
Fore Udder	.01 (.14)	.10 (.02)
Center	-.05 (.13)	.12 (.02)
Teats	.13 (.20)	.20 (.04)

[1]Standard errors are in parentheses.

bility. Traits receiving major emphasis in the program, such as basic form, would be most affected by this type of bias.

Mating to correct faults would also result in a dam with a five score being mated to a bull who sires excellent progeny while a dam with a one score would be mated to a bull who would correct faults on other traits. The offspring from the first mating might have a three score while the offspring of the second a one or a two. This would tend to reduce the daughter-dam regression coefficient and result in lowered heritability estimates.

The daughter-dam estimates support the hypothesis of possible bias on the part of the evaluator for basic form, scale and body. Sequential sums of squares for the daughter-dam analyses also showed significant sire differences for all traits at the .0001 level. Thus, sire differences are present in the data which may be genetic or may be evaluator and mating system inflated. Any bias which exists would be magnified when the sire component of variance is multiplied by four.

Using paternal half-sib estimates from the milk cow subset the structural traits were found to be moderately to highly heritable, feet and legs to be moderately heritable, and the udder traits lower in heritability. These generalizations are consistent with expectations based on former studies.

Heritabilities from the heifer and dry cow subsets (Table 16) are not always consistent with the milk cow subset. Basic form again shows an exceptionally high heritability estimate for both subsets (.81 for dry cows and .94 for heifers). Scale, front, feet and center support are

consistent across the three subset. Body is consistent for the milk cow and heifer subsets (.54 in each case) but considerably lower (.27) for the dry cow subset. Estimates for back, legs, rump, rear udder, fore udder and teats tend to vary across subsets. For the dry cow subset, heritability estimates for the udder traits are larger than estimates for the milk cow subset. Smaller numbers in the dry cow and heifer data sets may account for some of the inconsistency.

Heritability Adjustments

Heritabilities were adjusted for the effects of discontinuity using the methods of Vinson et al. (1976b). Adjustment caused most heritability estimates to be increased by 10 to 15 percent. Thus, the already exceptionally high estimates for basic form were increased to .98 for the milk cow subset, 1.05 for the dry cow subset and 1.18 for the heifer subset. Other adjusted estimates are listed in Table 16.

Because the mating specialist only has the discrete scores to work with, estimates obtained from the discrete scale are of the most practical value. In other words, the specialist needs to know what percentage of the variation in scores available to him is genetic. Adjustment puts estimates obtained from different discrete scales on a common basis, thereby allowing comparison. Thus, adjusted estimates are of more scientific than practical interest.

Phenotypic Correlations

Phenotypic correlations express the degree of relationship between two traits. The phenotypic correlations listed in Table 18 are the within

Table 18. Phenotypic (above diagonal) and genetic (below diagonal) correlations of M.A.P. data

	milk cow subset				
	1	2	3	4	5
1. Basic Form		-.080	-.289	-.187	-.025
2. Scale	-.055		.234	.012	.122
3. Front	-.706	.328		.222	.112
4. Body	-.566	-.105	.500		.228
5. Back	-.285	.316	.389	.519	
6. Legs	-.392	-.098	.352	.715	.394
7. Feet	-.291	.147	.390	.554	.290
8. Rump	-.312	-.438	-.005	.366	-.106
9. Rear Udder	-.319	-.132	-.030	-.004	-.410
10. Fore Udder	-.147	-.125	-.032	-.091	-.389
11. Center	-.026	.166	.297	.132	.188
12. Teats	.227	.198	-.147	-.349	-.074

6	7	8	9	10	11	12
-.108	-.062	-.056	-.092	-.065	.030	.032
.049	.082	.001	.018	.026	.020	.027
.140	.074	.096	.064	.044	.015	.011
.142	.084	.110	.044	.049	.047	-.003
.092	.057	.154	.022	.007	.019	.011
	.398	.113	.124	.087	.073	.037
.895		.113	.091	.070	.052	.042
-.022	.017		.126	.115	.073	.080
.030	-.162	.127		.434	.324	.302
-.052	-.176	.111	.826		.285	.388
.242	.284	-.178	.187	.416		.454
-.252	-.162	-.200	.116	.534	.607	

Table 18. Continued

	dry cow subset				
	1	2	3	4	5
1. Basic Form		-.093	-.188	-.113	.017
2. Scale	.205		.267	-.069	.024
3. Front	-.705	.290		.180	.085
4. Body	-.615	-.304	.158		.219
5. Back	-.464	-.089	.206	.294	
6. Legs	-.460	.216	.815	.788	.870
7. Feet	.588	-.163	.376	.609	.631
8. Rump	.791	-.915	-.999	-.011	-.221
9. Rear Udder	-.164	.223	.373	-.178	.097
10. Fore Udder	.201	.642	.586	-.336	-.172
11. Center	-.115	.285	.883	-.403	-.024
12. Teats	.145	.245	.534	-.395	-.010

6	7	8	9	10	11	12
-.122	-.121	.031	-.134	-.053	-.030	.030
.135	.103	.058	.102	.112	.094	.084
.176	.086	.074	.147	.102	.087	.092
.134	.099	.012	.041	.057	.040	-.012
.080	.038	.142	-.023	.039	.090	.089
	.434	.094	.100	.133	.069	.079
.811		.107	.060	.092	.069	.030
.167	-.595		.094	.090	.082	.099
-.012	.071	.669		.513	.473	.394
-.251	-.093	-.239	1.079		.397	.456
.194	.280	-.110	.787	.904		.580
.003	-.349	-.052	.634	.864	.909	

Table 18. Continued

heifer subset	1	2	3
1. Basic Form		-.050	-.312
2. Scale	.295		.230
3. Front	-.585	.284	
4. Body	-.830	.321	.680
5. Back	.000	.000	.000
6. Legs	-.894	.609	1.133
7. Feet	-.646	.203	.360
8. Rump	-.337	-.304	.445

4	5	6	7	8
-.356	-.043	-.070	-.054	-.087
.009	.156	.048	.068	-.044
.267	.196	.154	.180	.210
	.154	.060	.100	.071
.000		.145	.139	.162
.954	.000		.429	.235
.703	.000	.054		.119
.164	.000	.933	-.105	

herd and parity correlations obtained from the least squares analysis (ie)

$$\hat{p}_{ij} = (\sigma_{s_i s_j} + \sigma_{e_i e_j}) / \sqrt{(\sigma^2_{s_i} + \sigma^2_{e_i})(\sigma^2_{s_j} + \sigma^2_{e_j})}$$

where

$\sigma_{s_i s_j}$ = sire component of covariance between ith and jth traits

$\sigma_{e_i e_j}$ = error component of covariance

σ_{s_i} = sire component of variance for the ith trait

σ_{e_i} = error component of variance for the ith trait

Correlations were found to range from -.289 to .454 for the milk cow subset. Phenotypic correlations of all traits with basic form were found to be negative or only slightly positive. To interpret these correlations one must remember that a score of five for basic form represents a very thick animal. A negative correlation would then be interpreted as very angular cows tend to score undesirable (higher) on the correlated trait while thick cows tend to score desirable (lower) on the correlated trait. Front (-.289), body (-.187) and legs (-.108) produced the largest correlations with basic form. For both the milk cow and dry cow subsets, correlations with an absolute value greater than .081 are significantly different from zero at .01 level.

All correlations between the other eleven traits are positive except body with teats (-.003). In general, traits in close physical proximity have the largest correlations while traits in less close proximity have the smallest correlations. The udder traits are highly correlated with each other producing some of the largest correlations in the data; for the milk cow subset correlations are .454 center with teats, .434 fore with

rear udder, .388 teats with fore udder, .324 center with rear udder, .302 teats with rear udder and .285 center with fore udder. Correlation for feet with legs, .398 for the milk cow subset, .434 for the dry cow subset, and .429 for the heifer subset, are also among the largest correlations in their respective subsets.

Correlations for rump, legs and feet with rear udder and fore udder are significant at the .01 level, correlations with rear udder being larger than those with fore udder. Again, traits in close physical proximity have relatively larger correlations. Correlations coefficients are consistent across the three subsets.

Phenotypic correlations from this study are of similar magnitude to those obtained by Aitchison et al. (1972). Results of this study agree with Rennie et al. (1974) but are slightly smaller than results reported by Atkeson et al. (1969), Cassell et al. (1973) and Johnson and Fourt (1960).

Genetic Correlations

Genetic correlations express the degree of relationship between the additive genetic fractions of the total phenotypic variation. A positive genetic correlation indicates that selection for one trait will result in improvement in the correlated trait without direct selection for the correlated trait. Thus, a negative correlation indicates selection on one trait will change the correlated trait in the opposite direction. The expected correlated response was discussed in the literature review.

Genetic correlations (Table 18) are, in general, larger in magnitude than corresponding phenotypic correlations. Correlation for the milk cow subset range from -.706 to .895. Rennie et al. (1974), Cassell et al. (1973), Atkeson et al. (1969) and Johnson and Fourt (1960) all reported genetic correlations to be larger in magnitude than phenotypic correlations.

Again, all traits except teats were negatively correlated with basic form for the milk cow subset. However, scale, feet, rump and fore udder for the dry cow subset and scale for the heifer subset show positive genetic correlations with basic form. Negative correlations with basic form are again interpreted as selection for thicker cows results in a more desirable (lower) score on the correlated trait.

Several genetic correlations among the other eleven traits are negative, which is biologically undesirable. Notably, all body traits except scale are negatively correlated with teats in the milk cow subset. All body traits except scale and front show a negative correlation with basic form in the dry cow subset. The milk cow and dry cow subsets show several other negative genetic correlations which are not consistent across subsets. The heifer subset shows only two negative genetic correlations, rump with scale and rump with feet.

Exceedingly high genetic correlations of .895 for feet with legs and .826 for rear udder with fore udder are found in the milk cow subset. Corresponding values of .811 and 1.079 are found in the dry cow subset. Fore udder with center support (.904), center support with teats (.909), legs with back (.870), and center support with front (.833) also show

correlations greater than .300 in the dry cow subset. Results for the milk cow subset again show large positive correlations for traits in close physical proximity. The dry cow subset shows the same type of result, however, some traits not in close physical proximity show large positive correlations, center support with front being one example. Except for the negative correlations with basic form, results for the heifer subset show little consistency with the dry cow and milk cow subsets.

Genetic correlations obtained from this study are slightly smaller than results of other recent studies, Rennie et al. (1974), Cassell et al. (1973) and Atkeson et al. (1969). Also, the three above studies reported all genetic correlations to be positive. However, other studies, Freeman and Dunbar (1955) and Butcher et al. (1963), have reported negative genetic correlations.

Subscore Heritabilities

Subscore data for the dry cow and heifer data subsets were not analyzed because of insufficient data. Subscore data for the milk cow subset was edited in the same manner as the trait score data leaving one unique file for each of the seven traits with subscores. Editing left file sizes of 1,071 records for front, 373 records for legs, 560 records for feet, 430 records for rump, 547 records for rear udder, 673 records for fore udder and 513 records for teats. Trinomial breakdowns were generated for each file which was then analyzed using the milk cow model developed for the trait score data. Heritability estimates, their standard error, and adjustment to the normal scale are listed in Table 19.

Table 19. Heritabilities, standard errors, and corrected heritabilities for the subscore breakdowns

Trait: Front				Trait: Rear Udder			
breakdown	h^2	S.E.	cor.	breakdown	h^2	S.E.	cor.
Low Front	.07	.07	.11	Low Attachment	.12	.17	.37
Wing Shoulders	.07	.07	.14	Narrow Attachment	.01	.16	.01
Narrow Front	.10	.08	.16	Uneven Curvature	.07	.17	.13
Weak Crop	.34	.12	.81	Too Deep-Tilted	.01	.16	.02
Coarse	.12	.08	.41	Too Shallow-Tilted[1]			

[1]Insufficient data for this subscore.

Table 19. continued

Trait: Legs				Trait: Rump[2]		
breakdown	h^2	S.E.	cor.	breakdown	h^2	S.E.
Too Straight	.05	.28	.09	High Tail Head	-.13	.18
Too Much Set	.00	.27	.00	Sloping	-.43	.15
Hocks In	.28	.30	.47	Ridgy	-.08	.19
Stance	.44	.31	.89	Narrow	-.08	.19
Toes Out In Front	.35	.30	1.32			

[2]Corrected heritabilities not calculated for rump because of negative estimates for this trait.

Table 19. continued

Trait: Teats				Trait: Feet			
breakdown	h^2	S.E.	cor.	breakdown	h^2	S.E.	cor.
Wide Front Teats	.23	.19	.88	Shallow Heel	.47	.23	1.52
Too Large or Long	.11	.17	.15	Spread Toes	.59	.24	.93
Poorly Shaped	.60	.22	1.38	Faulty Pasterns	.18	.21	.34
Back Too Far	.31	.20	1.05	Toes Curl	.39	.22	.82
Too Close on Side	.52	.21	1.00				
Teats Strut[1]							

Table 19. continued

breakdown	Trait: Fore Udder h^2	S.E.	cor.
Weak Attachment	.30	.15	.47
Bulgy and Loose	.02	.12	.04
Too Deep-Tilted	-.10	.10	-.20
Too Shallow-Tilted	.10	.13	.17
Too Short	.15	.13	.92

Heritability estimates for the breakdowns for front, rear udder and fore udder are small in magnitude ranging from -.10 to .34. Breakdowns for legs are of small to moderate magnitude while breakdowns for feet and teats are of moderate to large magnitude. Several breakdowns including all four for rump have negative estimates. However, in all cases except "sloping" for rump the standard error of the estimate encompasses zero heritability. Assuming the true estimate for any trait is zero, this true estimate would be outside a 95 percent confidence interval one out of twenty times. Thus, the true estimate for "sloping" could be zero even though zero falls outside of a 95 percent confidence interval on the estimate. As no errors were found in the analysis procedure, negative estimates can be attributed to chance, the model or assumptions not fitting the data. However, the models used seem to characterize most traits thus these results can best be attributed to chance.

For legs, two of the more severe faults, "too straight" and "too much set," have very low heritability estimates, .05 and .00, respectively. Rear udder, fore udder, front and teats also have small estimates for the more severe faults (Table 20). For feet, the two relatively more severe faults "toes curl" and "faulty pasterns" are moderately heritable, but have lower estimates than the less severe faults. Thus, the more severe faults tend to have the lower heritability estimates.

Most of the descriptive codes found to be highly heritable by LaSalle et al. (1973) are lowly heritable in this study. The low estimates for fore and rear udder breakdowns do not agree with the work of VanVleck (1964). However, heritability estimates of the breakdowns for front do agree with VanVleck's study. Also, the assignment of subscores

Table 20. Heritability estimates for the relatively more severe subscores

Trait	Subscore	Hert.	S.E.
Front	Low Front	.07	.07
	Wing Shoulders	.07	.07
Feet	Faulty Pasterns	.18	.21
	Toes Curl	.39	.22
Legs	Too Straight	.05	.28
	Too Much Set	.00	.27
	Stance	.44	.31
Rump	Sloping	-.43	.15
Rear Udder	Low Attachment	.12	.17
	Too Deep-Tilted	.01	.16
Fore Udder	Too Shallow-Tilted	.10	.13
Teats	Too Long or Large	.11	.17
	Teats Strut[1]		

[1]Estimate not calculated because of insufficient data.

to only poor scoring animals rather than all animals may have some influence on the estimates in this study.

Subscore heritability estimates were adjusted to the normal scale even though the trinomial data do not have an underlying normal distribution. Trinomial scores were generated from data which came from a truncated normal distribution. Also, the method of generating trinomial scores resulted in a high percentage of zeros for each breakdown. What effect negating the assumption of normality has on the adjustments is unknown. Possibly the adjustments should not have been made, however, results are listed in Table 19. The adjustments should be viewed with the above problem in mind.

SUMMARY

Population parameters were estimated for the MAP program of Midwest Breeders Cooperative. These data were collected as a part of the MAP program after revisions based on an earlier analysis by Aitchison (1971). Revisions included a change in the coding of basic form, splitting the old single score for feet and legs into two separate scores, the addition of the trait teats while dropping size, disposition and milk out, addition of parity and stage of lactation information and the addition of descriptive subscores for certain traits. The purpose of the subcodes was to describe the nature of the fault resulting in an undesirable score.

Means and standard deviations for most traits changed little over the five years between data collections. Means for basic form, front, fore udder and center support being exceptions. Phenotypic correlations between traits from the present study were also in agreement with those from the earlier MAP analyses. However, heritability estimates based on a paternal half-sib analysis were somewhat different between the two studies, estimates ranged from .10 to .83 for milk cows in the present study. Part of this difference can be attributed to the more complete model used in the present study.

Heritability estimates obtained from a daughter-dam regression indicate difficulty in obtaining an estimate of the additive genetic variance. Bias in scoring induced by prior knowledge of the sire of the animal being score, negative assortative mating and the mating of a sire to a certain type of cow may account for the discrepancy. Further research is needed to locate the nature of the problem.

The models used in the present study required the data be analyzed in three subsets; milk cows, dry cows and heifers. Phenotypic correlations were consistent across subsets, however, means and standard deviations varied slightly across subsets. Phenotypic correlations for the milk cow subset ranged from -.289 to .454. All phenotypic correlations with the exceptions of those with basic form were positive most ranging from .00 to .20. Heritability estimates and genetic correlations were found to vary to a larger extent across subsets.

The analyses showed that the addition of parity and stage effects are necessary for an accurate model for the milk cow subset. However, parity adjustments are not necessary for dry cows. Differences were found in the severity of faults or subcodes. Heritability estimates for subcodes indicate that the more severe faults often have the lowest heritabilities.

Heritability estimates for both the traits scores and subcodes were adjusted for the effects of discontinuity. However, unadjusted heritability estimates would be used in most practical applications. The paternal half-sib heritability estimates indicate that improvement can be made toward more desirable trait scores. Subcode estimates indicate that improvement can be made in correcting certain faults, however, the possibility for correcting the more severe faults is more limited by their low heritability estimates. Genetic correlations indicate that selection for thicker cows will result in more desirable scores for most conformation traits. Also, selection for most traits will result in more desirable scores on traits in close physical proximity. Thus, the genetic basis for corrective mating is available but limited in certain cases.

BIBLIOGRAPHY

Aitchison, T. E. 1971. Evaluation of a type appraisal program in Holsteins. M.S. Thesis. Iowa State University, Ames, Iowa.

Aitchison, T. E., A. E. Freeman, and G. M. Thomson. 1972. Evaluation of a type appraisal program in Holsteins. J. Dairy Sci. 55: 840-844.

Allaire, F. R., H. E. Sterwert, and T. M. Ludwick. 1977. Variations in removal reasons and culling rates with age for dairy females. J. Dairy Sci. 60: 254-267.

Atkeson, G. W., G. E. Meadows, and L. D. McGillard. 1969. Weighting components of type in classifying Holsteins. J. Dairy Sci. 52: 1638-1642.

Benson, R. H., W. J. Tyler, and G. Hyatt. 1951. Some causes of variation in type ratings of Ayrshire cows. J. Dairy Sci. 34: 502. (Abstr.)

Butcher, D. E., R. G. Mitchell, I. D. Potterfield, and R. S. Dunbar, Jr. 1963. Heritability, phenotypic and genetic correlations between type ratings and milk fat production in Ayrshire cattle. J. Dairy Sci. 46: 971-975.

Carter, H. W., R. C. Rennie, and E. B. Burnside. 1965. Causes of variation in type classification data. J. Dairy Sci. 48: 790. (Abstr.)

Cassell, B. G., J. M. White, W. E. Vinson, and R. H. Kliewer. 1973. Genetic and phenotypic relationships among type traits in Holstein-Friesian cattle. J. Dairy Sci. 56: 1171-1177.

Dickinson, F. N., R. L. Powell, and H. D. Norman. 1976. An introduction to the USDA-DHIA Modified Contemporary Comparison. USDA Production Research Report No. 165.

Falconer, D. S. 1960. Introduction to quantitative genetics. The Ronald Press Company, New York.

Freeman, A. E., and R. S. Dunbar, Jr. 1955. Genetic analysis of the components of type conformation and production in Ayrshire cows. J. Dairy Sci. 38: 428-437.

Granthom, J. A., Jr., J. M. White, W. E. Vinson, and R. H. Kliewer. 1974. Genetic relationships between milk production and type in Holsteins. J. Dairy Sci. 57: 1483-1488.

Hansen, L. R., G. R. Barr, and D. A. Wiekert. 1969. Effect of age and stage of lactation on type classification. J. Dairy Sci. 52: 646-650.

Harvey, W. R. 1975. Least squares analysis of data with unequal subclass numbers. USDA Publication ARS H-4.

Harvey, W. R., and J. L. Lush. 1952. Genetic correlations between type and production in Jersey cattle. J. Dairy Sci. 35: 199-213.

Henderson, C. R. 1953. Estimation of variance and covariance components. Biometrics 9: 226-252.

Hillers, J. K., and D. O. Everson. 1972. Effects of various discrete distributions on the magnitude of heritability. J. Dairy Sci. 55: 682. (Abstr.)

Johnson, K. R., and D. L. Fourt. 1960. Heritability, genetic and phenotypic correlations of type, certain components of type, and production of Brown Swiss cattle. J. Dairy Sci. 43: 975-981.

LaSalle, T. J., J. W. Jamison, and J. M. White. 1973. Heritability of descriptive type traits in Holstein cattle. J. Dairy Sci. 56: 676. (Abstr.)

Legates, J. E. 1971. Components of variance for descriptive type classification of Holstein-Friesian cows. J. Dairy Sci. 54: 775. (Abstr.)

Lentz, W. E., P. D. Miller, and C. R. Henderson. 1969. Evaluating dairy sires by direct comparison. Unpublished paper presented at the American Society of Animal Science meeting, Purdue University, Lafayette, Indiana.

Norman, H. D., and L. D. VanVleck. 1970. Causes of variation in type appraisal traits. J. Dairy Sci. 53: 665. (Abstr.)

Norman, H. D., and L. D. VanVleck. 1972. Type appraisal: II. Variation in type due to sires, herds, and years. J. Dairy Sci. 55: 1717-1725.

O'Bleness, G. V., L. D. VanVleck, and C. R. Henderson. 1960. Heritabilities of some type appraisal traits and their genetic and phenotypic correlations with production. J. Dairy Sci. 43: 1490-1498.

Prescott, M. S., M. Scholl, H. H. Wing, and W. A. Prescott. 1960. Holstein-Friesian history. The Corse Press, Sandy Creek, New York.

Rennie, J. C., T. R. Batra, M. G. Freeman, J. W. Wilton, and E. B. Burnside. 1974. Environmental and genetic parameters for type traits in Holstein cows. J. Dairy Sci. 57: 1221-1224.

Rindsig, G. L. 1976. Using a bull's pedigree in mixed model sire evaluation. Ph.D. Thesis. Iowa State University, Ames, Iowa.

Specht, L. W., H. W. Carter, and L. D. VanVleck. 1967. First classification scores and length of herd life. J. Dairy Sci. 50: 1690-1694.

Swiger, L. A., W. R. Harvey, D. O. Everson, and K. E. Gregory. 1964. The variance of the intraclass correlation involving groups with one observation. Biometrics 20: 818-826.

Touchberry, R. W. and K. R. Tabler. 1951. The changes in the type ratings of Holstein and Guernsey cows when rated by the same three judges at two consecutive times. J. Animal Sci. 10: 1029.

VanVleck, L. D. 1964. Variation in type appraisal scores due to sire and herd effects. J. Dairy Sci. 47: 1249-1256.

VanVleck, L. D. 1972. Estimation of heritability of threshold characters. J. Dairy Sci. 55: 218-225.

VanVleck, L. D., and H. D. Norman. 1972. Association of type traits and reason for disposal. J. Dairy Sci. 55: 1698-1705.

Vinson, W. E., J. M. White, B. L. Combs, and R. H. Kliewer. 1976a. Sources of variation in Holstein descriptive classification traits. J. Dairy Sci. 59: 522-526.

Vinson, W. E., J. M. White, and R. H. Kliewer. 1976b. Overall classification as a selection criterion for improving categorically scored components of type in Holsteins. J. Dairy Sci. 59: 2104-2114.

White, J. M. 1974. Genetic parameters of conformational and management traits. J. Dairy Sci. 57: 1267-1278.

White, J. M., and W. E. Vinson. 1976. Type in the Holstein-Friesian breeding program. Paper presented at the convention of the Holstein-Friesian Association of America, Philadelphia, Pennsylvania, July 1, 1976.

Wilcox, C. J., R. F. Mater, K. O. Pfau, R. F. Gabriel, and J. W. Barlett. 1959. Changes in type ratings of Holstein cows due to age, season, stage of lactation, classifier and year. J. Dairy Sci. 42: 1867-1876.

Wilcox, C. J., S. N. Gaunt, and B. R. Farthing. 1971. Genetic interrelationships of milk composition and yield. Southern Cooperative Series Bulletin No. 155, March 1971.

ACKNOWLEDGMENTS

First, I wish to express special appreciation to Dr. A. E. Freeman for his serving as my major professor and the many hours he spent helping me with this manuscript. I would like to extend very special thanks to my fellow graduate students, a group whose assistance is often overlooked. Special thanks also go to Dr. P. J. Berger for his assistance in programming and serving on my committee.

Appreciation is also expressed to Drs. D. F. Cox and R. L. Willham for serving on my graduate committee. Last, I wish to thank all my friends who provided companionship during the preparation of this manuscript.